

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Adema, Gosse Jan
Meygaard, Linde
Gorman, Daniel M.
McClanahan, Terrill K.
Zurawski, Sandra M.
Zurawski, Gerard
Lanier, Lewis L.
Phillips Jr., Joseph H.
- (ii) TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
Related Reagents
- (iii) NUMBER OF SEQUENCES: 22
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DNAX Research Institute
 - (B) STREET: 901 California Avenue
 - (C) CITY: Palo Alto
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94304-1104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/985,950
 - (B) FILING DATE: 05-DEC-1997
 - (C) CLASSIFICATION: Utility
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/041,279
 - (B) FILING DATE: 21-MARCH-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/033,181
 - (B) FILING DATE: 16-DEC-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/032,252
 - (B) FILING DATE: 06-DEC-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ching, Edwin P.
 - (B) REGISTRATION NUMBER: 34,090
 - (C) REFERENCE/DOCKET NUMBER: DX0670K
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (650)852-9196
 - (B) TELEFAX: (650)496-1204

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650)852-9196

(B) TELEFAX: (650)496-1204

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1249 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 154..1062

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 211..1062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTTTGGGGAA GGCTCCTGGC CCCACAGCC CTCTTCGGAG CCTGAGCCCG GCTCTCCTCA	60
CTCACCTCAA CCCCCAGGCG GCCCCTCCAC AGGGCCCTC TCCTGCCTGG ACGGCTCTGC	120
TGGTCTCCCC GTCCCCTGGA GAAGAACAAG GCC ATG GGT CGG CCC CTG CTG CTG	174
Met Gly Arg Pro Leu Leu Leu	
-19 -15	
CCC CTA CTG CCC CTG CTG CTG CCG CCA GCA TTT CTG CAG CCT AGT GGC	222
Pro Leu Leu Pro Leu Leu Leu Pro Pro Ala Phe Leu Gln Pro Ser Gly	
-10 -5 1	
TCC ACA GGA TCT GGT CCA AGC TAC CTT TAT GGG GTC ACT CAA CCA AAA	270
Ser Thr Gly Ser Gly Pro Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys	
5 10 15 20	
CAC CTC TCA GCC TCC ATG GGT GGC TCT GTG GAA ATC CCC TTC TCC TTC	318
His Leu Ser Ala Ser Met Gly Gly Ser Val Glu Ile Pro Phe Ser Phe	
25 30 35	
TAT TAC CCC TGG GAG TTA GCC ACA GCT CCC GAC GTG AGA ATA TCC TGG	366
Tyr Tyr Pro Trp Glu Leu Ala Thr Ala Pro Asp Val Arg Ile Ser Trp	
40 45 50	
AGA CGG GGC CAC TTC CAC GGG CAG TCC TTC TAC AGC ACA AGG CCG CCT	414
Arg Arg Gly His Phe His Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro	
55 60 65	
TCC ATT CAC AAG GAT TAT GTG AAC CGG CTC TTT CTG AAC TGG ACA GAG	462
Ser Ile His Lys Asp Tyr Val Asn Arg Leu Phe Leu Asn Trp Thr Glu	

70	75	80	
GGT CAG AAG AGC GGC TTC CTC AGG ATC TCC AAC CTG CAG AAG CAG GAC Gly Gln Lys Ser Gly Phe Leu Arg Ile Ser Asn Leu Gln Lys Gln Asp 85 90 95 100			510
CAG TCT GTG TAT TTC TGC CGA GTT GAG CTG GAC ACA CGG AGC TCA GGG Gln Ser Val Tyr Phe Cys Arg Val Glu Leu Asp Thr Arg Ser Ser Gly 105 110 115			558
AGG CAG CAG TGG CAG TCC ATC GAG GGG ACC AAA CTC TCC ATC ACC CAG Arg Gln Gln Trp Gln Ser Ile Glu Gly Thr Lys Leu Ser Ile Thr Gln 120 125 130			606
GCT GTC ACG ACC ACC ACC CAG AGG CCC AGC AGC ATG ACT ACC ACC TGG Ala Val Thr Thr Thr Thr Gln Arg Pro Ser Ser Met Thr Thr Thr Trp 135 140 145			654
AGG CTC AGT AGC ACA ACC ACC ACA ACC GGC CTC AGG GTC ACA CAG GGC Arg Leu Ser Ser Thr Thr Thr Thr Gly Leu Arg Val Thr Gln Gly 150 155 160			702
AAA CGA CGC TCA GAC TCT TGG CAC ATA AGT CTG GAG ACT GCT GTG GGG Lys Arg Arg Ser Asp Ser Trp His Ile Ser Leu Glu Thr Ala Val Gly 165 170 175 180			750
GTG GCA GTG GCT GTC ACT GTG CTC GGA ATC ATG ATT TTG GGA CTG ATC Val Ala Val Ala Val Thr Val Leu Gly Ile Met Ile Leu Gly Leu Ile 185 190 195			798
TGC CTC CTC AGG TGG AGG AGA AGG AAA GGT CAG CAG CGG ACT AAA GCC Cys Leu Leu Arg Trp Arg Arg Arg Lys Gly Gln Gln Arg Thr Lys Ala 200 205 210			846
ACA ACC CCA GCC AGG GAA CCC TTC CAA AAC ACA GAG GAG CCA TAT GAG Thr Thr Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu 215 220 225			894
AAT ATC AGG AAT GAA GGA CAA AAT ACA GAT CCC AAG CTA AAT CCC AAG Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys 230 235 240			942
GAT GAC GGC ATC GTA TAT GCT TCC CTT GCC CTC TCC AGC TCC ACC TCA Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser 245 250 255 260			990
CCC AGA GCA CCT CCC AGC CAC CGT CCC CTC AAG AGC CCC CAG AAC GAG Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn Glu 265 270 275			1038
ACC CTG TAC TCT GTC TTA AAG GCC TAACCAATGG ACAGCCCTCT CAAGACTGAA Thr Leu Tyr Ser Val Leu Lys Ala 280			1092
TGGTGAGGCC AGGTACAGTG GCGCACACCT GTAATCCCAG CTACTCTGAA GCCTGAGGCA			1152
GAATCAAGTG AGCCCAGGAG TTCAGGGCCA GCTTTGATAA TGGAGCGAGA TGCCATCTCT			1212

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Pro Leu Leu Leu Pro Pro
-19          -15          -10          -5

Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro Ser Tyr Leu
      1              5              10

Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
    15              20              25

Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala
    30              35              40              45

Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
      50              55              60

Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
      65              70              75

Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile
      80              85              90

Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
    95              100             105

Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile Glu Gly
   110             115             120             125

Thr Lys Leu Ser Ile Thr Gln Ala Val Thr Thr Thr Thr Gln Arg Pro
      130             135             140

Ser Ser Met Thr Thr Thr Trp Arg Leu Ser Ser Thr Thr Thr Thr Thr
      145             150             155

Gly Leu Arg Val Thr Gln Gly Lys Arg Arg Ser Asp Ser Trp His Ile
      160             165             170

Ser Leu Glu Thr Ala Val Gly Val Ala Val Ala Val Thr Val Leu Gly
      175             180             185

Ile Met Ile Leu Gly Leu Ile Cys Leu Leu Arg Trp Arg Arg Arg Lys
   190             195             200             205

Gly Gln Gln Arg Thr Lys Ala Thr Thr Pro Ala Arg Glu Pro Phe Gln
      210             215             220

```

Asn Thr Glu Glu Pro Tyr Glu Asn Ile Arg Asn Glu Gly Gln Asn Thr
225 230 235

Asp Pro Lys Leu Asn Pro Lys Asp Asp Gly Ile Val Tyr Ala Ser Leu
240 245 250

Ala Leu Ser Ser Ser Thr Ser Pro Arg Ala Pro Pro Ser His Arg Pro
255 260 265

Leu Lys Ser Pro Gln Asn Glu Thr Leu Tyr Ser Val Leu Lys Ala
270 275 280

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 78..374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCCAGTGTG CCTAGACAGA GCATCCTTGC CTCCTGATG GCTTTGCTGA TCTCGCTTCC	60
CTGGAGGGGAC TCCAGCC ATG GCT CAG GTC CTG CTT CTG CTC TCA TCA GGC	110
Met Ala Gln Val Leu Leu Leu Ser Ser Gly	
1 5 10	
TGT CTG CAT GCT GGA AAT TCA GAA AGA TAC AAC AGA AAA AAT GGC TTT	158
Cys Leu His Ala Gly Asn Ser Glu Arg Tyr Asn Arg Lys Asn Gly Phe	
15 20 25	
GGG GTC AAC CAA CCT GAA CGC TGC TCT GGA GTC CAG GGT GGC TCC ATC	206
Gly Val Asn Gln Pro Glu Arg Cys Ser Gly Val Gln Gly Gly Ser Ile	
30 35 40	
GAC ATC CCC TTC TCC TTC TAT TTC CCC TGG AAG TTG GCC AAG GAT CCA	254
Asp Ile Pro Phe Ser Phe Tyr Phe Pro Trp Lys Leu Ala Lys Asp Pro	
45 50 55	
CAG ATG AGC ATA GCC TGG AAA TGG AAG GAT TTC CAT GGG GAA GTC ATC	302
Gln Met Ser Ile Ala Trp Lys Trp Lys Asp Phe His Gly Glu Val Ile	
60 65 70 75	
TAC AAC TCC TCC CTG CCT TTC ATA CAT GAG CAC TTC AAG GGC CGG CTC	350
Tyr Asn Ser Ser Leu Pro Phe Ile His Glu His Phe Lys Gly Arg Leu	
80 85 90	
ATC CTG AAC TGG ACA CAG GGT CAG AC	376

Ile Leu Asn Trp Thr Gln Gly Gln
95

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Gln Val Leu Leu Leu Ser Ser Gly Cys Leu His Ala Gly
1 5 10 15
Asn Ser Glu Arg Tyr Asn Arg Lys Asn Gly Phe Gly Val Asn Gln Pro
20 25 30
Glu Arg Cys Ser Gly Val Gln Gly Gly Ser Ile Asp Ile Pro Phe Ser
35 40 45
Phe Tyr Phe Pro Trp Lys Leu Ala Lys Asp Pro Gln Met Ser Ile Ala
50 55 60
Trp Lys Trp Lys Asp Phe His Gly Glu Val Ile Tyr Asn Ser Ser Leu
65 70 75 80
Pro Phe Ile His Glu His Phe Lys Gly Arg Leu Ile Leu Asn Trp Thr
85 90 95
Gln Gly Gln

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 155..1015

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1247
- (D) OTHER INFORMATION: /note= "nucleotide 1247 designated

C, but may be C or T"

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 218..1015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACCGGTCCGG AATTCCTCCGGG TCGACCCACG CGTCCGGGAA GCCCCATAGG CAGGAGGCC	60
CCGGGCAGCA CATCCTGTCT GCTTGTGTCT GCTGCAGAGT TCTGTCCTG CATTGGTGCG	120
CCTCAGGCCA GGCTGCACTG CTGGGACCTG GGCC ATG TCT CCC CAC CCC ACC	172
Met Ser Pro His Pro Thr	
-21 -20	
GCC CTC CTG GGC CTA GTG CTC TGC CTG GCC CAG ACC ATC CAC ACG CAG	220
Ala Leu Leu Gly Leu Val Leu Cys Leu Ala Gln Thr Ile His Thr Gln	
-15 -10 -5 1	
GAG GAA GAT CTG CCC AGA CCC TCC ATC TCG GCT GAG CCA GGC ACC GTG	268
Glu Glu Asp Leu Pro Arg Pro Ser Ile Ser Ala Glu Pro Gly Thr Val	
5 10 15	
ATC CCC CTG GGG AGC CAT GTG ACT TTC GTG TGC CGG GGC CCG GTT GGG	316
Ile Pro Leu Gly Ser His Val Thr Phe Val Cys Arg Gly Pro Val Gly	
20 25 30	
GTT CAA ACA TTC CGC CTG GAG AGG GAG AGT AGA TCC ACA TAC AAT GAT	364
Val Gln Thr Phe Arg Leu Glu Arg Glu Ser Arg Ser Thr Tyr Asn Asp	
35 40 45	
ACT GAA GAT GTG TCT CAA GCT AGT CCA TCT GAG TCA GAG GCC AGA TTC	412
Thr Glu Asp Val Ser Gln Ala Ser Pro Ser Glu Ser Glu Ala Arg Phe	
50 55 60 65	
CGC ATT GAC TCA GTA AGT GAA GGA AAT GCC GGG CCT TAT CGC TGC ATC	460
Arg Ile Asp Ser Val Ser Glu Gly Asn Ala Gly Pro Tyr Arg Cys Ile	
70 75 80	
TAT TAT AAG CCC CCT AAA TGG TCT GAG CAG AGT GAC TAC CTG GAG CTG	508
Tyr Tyr Lys Pro Pro Lys Trp Ser Glu Gln Ser Asp Tyr Leu Glu Leu	
85 90 95	
CTG GTG AAA GAA ACC TCT GGA GGC CCG GAC TCC CCG GAC ACA GAG CCC	556
Leu Val Lys Glu Thr Ser Gly Gly Pro Asp Ser Pro Asp Thr Glu Pro	
100 105 110	
GGC TCC TCA GCT GGA CCC ACG CAG AGG CCG TCG GAC AAC AGT CAC AAT	604
Gly Ser Ser Ala Gly Pro Thr Gln Arg Pro Ser Asp Asn Ser His Asn	
115 120 125	
GAG CAT GCA CCT GCT TCC CAA GGC CTG AAA GCT GAG CAT CTG TAT ATT	652
Glu His Ala Pro Ala Ser Gln Gly Leu Lys Ala Glu His Leu Tyr Ile	
130 135 140 145	
CTC ATC GGG GTC TCA GTG GTC TTC CTC TTC TGT CTC CTC CTC CTG GTC	700
Leu Ile Gly Val Ser Val Val Phe Leu Phe Cys Leu Leu Leu Leu Val	
150 155 160	

Cys Arg Gly Pro Val Gly Val Gln Thr Phe Arg Leu Glu Arg Glu Ser
 30 35 40
 Arg Ser Thr Tyr Asn Asp Thr Glu Asp Val Ser Gln Ala Ser Pro Ser
 45 50 55
 Glu Ser Glu Ala Arg Phe Arg Ile Asp Ser Val Ser Glu Gly Asn Ala
 60 65 70 75
 Gly Pro Tyr Arg Cys Ile Tyr Tyr Lys Pro Pro Lys Trp Ser Glu Gln
 80 85 90
 Ser Asp Tyr Leu Glu Leu Leu Val Lys Glu Thr Ser Gly Gly Pro Asp
 95 100 105
 Ser Pro Asp Thr Glu Pro Gly Ser Ser Ala Gly Pro Thr Gln Arg Pro
 110 115 120
 Ser Asp Asn Ser His Asn Glu His Ala Pro Ala Ser Gln Gly Leu Lys
 125 130 135
 Ala Glu His Leu Tyr Ile Leu Ile Gly Val Ser Val Val Phe Leu Phe
 140 145 150 155
 Cys Leu Leu Leu Leu Val Leu Phe Cys Leu His Arg Gln Asn Gln Ile
 160 165 170
 Lys Gln Gly Pro Pro Arg Ser Lys Asp Glu Glu Gln Lys Pro Gln Gln
 175 180 185
 Arg Pro Asp Leu Ala Val Asp Val Leu Glu Arg Thr Ala Asp Lys Ala
 190 195 200
 Thr Val Asn Gly Leu Pro Glu Lys Asp Arg Glu Thr Asp Thr Ser Ala
 205 210 215
 Leu Ala Ala Gly Ser Ser Gln Glu Val Thr Tyr Ala Gln Leu Asp His
 220 225 230 235
 Trp Ala Leu Thr Gln Arg Thr Ala Arg Ala Val Ser Pro Gln Ser Thr
 240 245 250
 Lys Pro Met Ala Glu Ser Ile Thr Tyr Ala Ala Val Ala Arg His
 255 260 265

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 69..929

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 132..929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAAGGCTGCA GAGTTCTGTC CTTGCATTGG TGCGCCTCAG GCCAGGCTGC ACTGCTGGGA	60
CCTGGGCC ATG TCT CCC CAC CCC ACC GCC CTC CTG GGC CTA GTG CTC TGC	110
Met Ser Pro His Pro Thr Ala Leu Leu Gly Leu Val Leu Cys	
-21 -20 -15 -10	
CTG GCC CAG ACC ATC CAC ACG CAG GAG GAA GAT CTG CCC AGA CCC TCC	158
Leu Ala Gln Thr Ile His Thr Gln Glu Glu Asp Leu Pro Arg Pro Ser	
-5 1 5	
ATC TCG GCT GAG CCA GGC ACC GTG ATC CCC CTG GGG AGC CAT GTG ACT	206
Ile Ser Ala Glu Pro Gly Thr Val Ile Pro Leu Gly Ser His Val Thr	
10 15 20 25	
TTC GTG TGC CGG GGC CCG GTT GGG GTT CAA ACA TTC CGC CTG GAG AGG	254
Phe Val Cys Arg Gly Pro Val Gly Val Gln Thr Phe Arg Leu Glu Arg	
30 35 40	
GAG AGT AGA TCC ACA TAC AAT GAT ACT GAA GAT GTG TCT CAA GCT AGT	302
Glu Ser Arg Ser Thr Tyr Asn Asp Thr Glu Asp Val Ser Gln Ala Ser	
45 50 55	
CCA TCT GAG TCA GAG GCC AGA TTC CGC ATT GAC TCA GTA AGT GAA GGA	350
Pro Ser Glu Ser Glu Ala Arg Phe Arg Ile Asp Ser Val Ser Glu Gly	
60 65 70	
AAT GCC GGG CCT TAT CGC TGC ATC TAT TAT AAG CCC CCT AAA TGG TCT	398
Asn Ala Gly Pro Tyr Arg Cys Ile Tyr Tyr Lys Pro Pro Lys Trp Ser	
75 80 85	
GAG CAG AGT GAC TAC CTG GAG CTG CTG GTG AAA GAA ACC TCT GGA GGC	446
Glu Gln Ser Asp Tyr Leu Glu Leu Leu Val Lys Glu Thr Ser Gly Gly	
90 95 100 105	
CCG GAC TCC CCG GAC ACA GAG CCC GGC TCC TCA GCT GGA CCC ACG CAG	494
Pro Asp Ser Pro Asp Thr Glu Pro Gly Ser Ser Ala Gly Pro Thr Gln	
110 115 120	
AGG CCG TCG GAC AAC AGT CAC AAT GAG CAT GCA CCT GCT TCC CAA GGC	542
Arg Pro Ser Asp Asn Ser His Asn Glu His Ala Pro Ala Ser Gln Gly	
125 130 135	
CTG AAA GCT GAG CAT CTG TAT ATT CTC ATC GGG GTC TCA GTG GTC TTC	590
Leu Lys Ala Glu His Leu Tyr Ile Leu Ile Gly Val Ser Val Val Phe	
140 145 150	
CTC TTC TGT CTC CTC CTC CTG GTC CTC TTC TGC CTC CAT CGC CAG AAT	638
Leu Phe Cys Leu Leu Leu Leu Val Leu Phe Cys Leu His Arg Gln Asn	

155	160	165	
CAG ATA AAG CAG GGG CCC CCC AGA AGC AAG GAC GAG GAG CAG AAG CCA			686
Gln Ile Lys Gln Gly Pro Pro Arg Ser Lys Asp Glu Glu Gln Lys Pro			
170	175	180	185
CAG CAG AGG CCT GAC CTG GCT GTT GAT GTT CTA GAG AGG ACA GCA GAC			734
Gln Gln Arg Pro Asp Leu Ala Val Asp Val Leu Glu Arg Thr Ala Asp			
	190	195	200
AAG GCC ACA GTC AAT GGA CTT CCT GAG AAG GAC AGA GAG ACG GAC ACC			782
Lys Ala Thr Val Asn Gly Leu Pro Glu Lys Asp Arg Glu Thr Asp Thr			
	205	210	215
TCG GCC CTG GCT GCA GGG AGT TCC CAG GAG GTG ACG TAT GCT CAG CTG			830
Ser Ala Leu Ala Ala Gly Ser Ser Gln Glu Val Thr Tyr Ala Gln Leu			
	220	225	230
GAC CAC TGG GCC CTC ACA CAG AGG ACA GCC CGG GCT GTG TCC CCA CAG			878
Asp His Trp Ala Leu Thr Gln Arg Thr Ala Arg Ala Val Ser Pro Gln			
	235	240	245
TCC ACA AAG CCC ATG GCC GAG TCC ATC ACG TAT GCA GCC GTT GCC AGA			926
Ser Thr Lys Pro Met Ala Glu Ser Ile Thr Tyr Ala Ala Val Ala Arg			
	250	255	260
CAC TGACCCCATATA CCCACCTGGC CTCTGCACCT GAGGGTAGAA AGTCACTCTA			979
His			
GGAAAAGCCT GAAGCAGCCA TTTGGAAGGC TTCCTGTTGG ATTCTCTTC ATCTAGAAAG			1039
CCAGCCAGGC AGCTGTCCTG GAGACAAGAG CTGGAGACTG GAGGTTTCTA ACCAGCATCC			1099
AGAAGGTTCG TTAGCCAGGT GGTCCCTTCT ACAATCGAGC AGCTCCTTGG ACAGACTGTT			1159
TCTCAGTTAT TTCCAGAGAC CCAGCTACAG TTCCCTGGCT GTTCTAGAG ACCCAGCTTT			1219
ATTCACCTGA CTGTTTCCAG AGACCCAGCT AAAGTCACCT GCCTGTTCTA AAGGCCCAGC			1279
TACAGCCAAT CAGCCGATTT CCTGAGCAGT GATGCCACCT CCAAGCTTGT CCTAGGTGTC			1339
TGCTGTGAAC CTCCAGTGAC CCCAGAGACT TTGCTGTAAT TATCTGCCCT GCTGACCCTA			1399
AAGACCTTCC TAGAAGTCAA GAGCTAGCCT TGAGACTGTG CTATACACAC ACAGCTGAGA			1459
GCCAAGCCCA GTTCTCTGGG TTGTGCTTTA CTCCACGCAT CAATAAATAA TTTTGAAGGC			1519
CTCACATCTG GCAGCCCCAG GCCTGGTCCT GGGTGTCATAG GTCTCTCGGA CCCACTCTCT			1579
GCCTTCACAG TTGTTCAAAG CTGAGTGAGG GAAACAGGAC TTACGAAAAC GTGTCAGCGT			1639
TTTCTTTTAA AAATTTAATT GATCAGGATT GTACGTAAAA AAAAAAAAAA AAAAAAAAAA			1699
AAAAAAAAAA AAAAAAAAAA AAAAAAAGG			1728

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Pro His Pro Thr Ala Leu Leu Gly Leu Val Leu Cys Leu Ala
-21 -20 -15 -10

Gln Thr Ile His Thr Gln Glu Glu Asp Leu Pro Arg Pro Ser Ile Ser
-5 1 5 10

Ala Glu Pro Gly Thr Val Ile Pro Leu Gly Ser His Val Thr Phe Val
15 20 25

Cys Arg Gly Pro Val Gly Val Gln Thr Phe Arg Leu Glu Arg Glu Ser
30 35 40

Arg Ser Thr Tyr Asn Asp Thr Glu Asp Val Ser Gln Ala Ser Pro Ser
45 50 55

Glu Ser Glu Ala Arg Phe Arg Ile Asp Ser Val Ser Glu Gly Asn Ala
60 65 70 75

Gly Pro Tyr Arg Cys Ile Tyr Tyr Lys Pro Pro Lys Trp Ser Glu Gln
80 85 90

Ser Asp Tyr Leu Glu Leu Leu Val Lys Glu Thr Ser Gly Gly Pro Asp
95 100 105

Ser Pro Asp Thr Glu Pro Gly Ser Ser Ala Gly Pro Thr Gln Arg Pro
110 115 120

Ser Asp Asn Ser His Asn Glu His Ala Pro Ala Ser Gln Gly Leu Lys
125 130 135

Ala Glu His Leu Tyr Ile Leu Ile Gly Val Ser Val Val Phe Leu Phe
140 145 150 155

Cys Leu Leu Leu Leu Val Leu Phe Cys Leu His Arg Gln Asn Gln Ile
160 165 170

Lys Gln Gly Pro Pro Arg Ser Lys Asp Glu Glu Gln Lys Pro Gln Gln
175 180 185

Arg Pro Asp Leu Ala Val Asp Val Leu Glu Arg Thr Ala Asp Lys Ala
190 195 200

Thr Val Asn Gly Leu Pro Glu Lys Asp Arg Glu Thr Asp Thr Ser Ala
205 210 215

Leu Ala Ala Gly Ser Ser Gln Glu Val Thr Tyr Ala Gln Leu Asp His
220 225 230 235

Trp Ala Leu Thr Gln Arg Thr Ala Arg Ala Val Ser Pro Gln Ser Thr
 240 245 250

Lys Pro Met Ala Glu Ser Ile Thr Tyr Ala Ala Val Ala Arg His
 255 260 265

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 568 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 24..428

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 87..428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCACGCGTCC GGGGACCGGG GCC ATG TCT CCA CAC CTC ACT GCT CTC CTG	50
Met Ser Pro His Leu Thr Ala Leu Leu	
-21 -20 -15	
GGC CTA GTG CTC TGC CTG GCC CAG ACC ATC CAC ACG CAG GAG GGG GCC	98
Gly Leu Val Leu Cys Leu Ala Gln Thr Ile His Thr Gln Glu Gly Ala	
-10 -5 1	
CTT CCC AGA CCC TCC ATC TCG GCT GAG CCA GGC ACT GTG ATC TCC CCG	146
Leu Pro Arg Pro Ser Ile Ser Ala Glu Pro Gly Thr Val Ile Ser Pro	
5 10 15 20	
GGG AGC CAT GTG ACT TTC ATG TGC CGG GGC CCG GTT GGG GTT CAA ACA	194
Gly Ser His Val Thr Phe Met Cys Arg Gly Pro Val Gly Val Gln Thr	
25 30 35	
TTC CGC CTG GAG AGG GAG GAT AGA GCC AAG TAC AAA GAT AGT TAT AAT	242
Phe Arg Leu Glu Arg Glu Asp Arg Ala Lys Tyr Lys Asp Ser Tyr Asn	
40 45 50	
GTG TTT CGA CTT GGT CCA TCT GAG TCA GAG GCC AGA TTC CAC ATT GAC	290
Val Phe Arg Leu Gly Pro Ser Glu Ser Glu Ala Arg Phe His Ile Asp	
55 60 65	
TCA GTA AGT GAA GGA AAT GCC GGG CTT TAT CGC TGC CTC TAT TAT AAG	338
Ser Val Ser Glu Gly Asn Ala Gly Leu Tyr Arg Cys Leu Tyr Tyr Lys	
70 75 80	
CCC CCT GGA TGG TCT GAG CAC AGT GAC TTC CTG GAG CTG CTG GTG AAA	386
Pro Pro Gly Trp Ser Glu His Ser Asp Phe Leu Glu Leu Leu Val Lys	

85	90	95	100	
GGG ACT GTG CCA GGC ACT GAA GCC TCC GGA TTT GAT GCA CCA				428
Gly Thr Val Pro Gly Thr Glu Ala Ser Gly Phe Asp Ala Pro				
105		110		
TGAATGAGGA GAAATGGCCT CCCGTCTTGT GAACTTCAAT GGGGAGAAAT AATTAGAATG				488
AGCAATAGAA ATGCACAGAT GCCTATACAT ACATATACAA ATAAAAAGAT ACGATTTCGCA				548
AAAAAAAAAA AAAAAAGGGC				568

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ser Pro His Leu Thr Ala Leu Leu Gly Leu Val Leu Cys Leu Ala																			
-21 -20					-15														-10
Gln Thr Ile His Thr Gln Glu Gly Ala Leu Pro Arg Pro Ser Ile Ser																			
-5					1					5									10
Ala Glu Pro Gly Thr Val Ile Ser Pro Gly Ser His Val Thr Phe Met																			
					15					20									25
Cys Arg Gly Pro Val Gly Val Gln Thr Phe Arg Leu Glu Arg Glu Asp																			
					30					35									40
Arg Ala Lys Tyr Lys Asp Ser Tyr Asn Val Phe Arg Leu Gly Pro Ser																			
					45					50									55
Glu Ser Glu Ala Arg Phe His Ile Asp Ser Val Ser Glu Gly Asn Ala																			
60					65					70									75
Gly Leu Tyr Arg Cys Leu Tyr Tyr Lys Pro Pro Gly Trp Ser Glu His																			
					80					85									90
Ser Asp Phe Leu Glu Leu Leu Val Lys Gly Thr Val Pro Gly Thr Glu																			
					95					100									105
Ala Ser Gly Phe Asp Ala Pro																			
					110														

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 81..1397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
GTCGACCCAC GCGTCCGCCT CTGTCCTGCC AGCACCGAGG GCTCATCCAT CCACAGAGCA      60
GTGCAGTGGG AGGAGACGCC ATG ACC CCC ATC CTC ACG GTC CTG ATC TGT      110
      Met Thr Pro Ile Leu Thr Val Leu Ile Cys
              1              5              10
CTC GGG CTG AGC CTG GAC CCC AGG ACC CAC GTG CAG GCA GGG CCC CTC      158
Leu Gly Leu Ser Leu Asp Pro Arg Thr His Val Gln Ala Gly Pro Leu
              15              20              25
CCC AAG CCC ACC CTC TGG GCT GAG CCA GGC TCT GTG ATC ACC CAA GGG      206
Pro Lys Pro Thr Leu Trp Ala Glu Pro Gly Ser Val Ile Thr Gln Gly
              30              35              40
AGT CCT GTG ACC CTC AGG TGT CAG GGG AGC CTG GAG ACG CAG GAG TAC      254
Ser Pro Val Thr Leu Arg Cys Gln Gly Ser Leu Glu Thr Gln Glu Tyr
              45              50              55
CAT CTA TAT AGA GAA AAG AAA ACA GCA CTC TGG ATT ACA CGG ATC CCA      302
His Leu Tyr Arg Glu Lys Lys Thr Ala Leu Trp Ile Thr Arg Ile Pro
              60              65              70
CAG GAG CTT GTG AAG AAG GGC CAG TTC CCC ATC CTA TCC ATC ACC TGG      350
Gln Glu Leu Val Lys Lys Gly Gln Phe Pro Ile Leu Ser Ile Thr Trp
              75              80              85
GAA CAT GCA GGG CGG TAT TGC TGT ATC TAT GGC AGC CAC ACT GCA GGC      398
Glu His Ala Gly Arg Tyr Cys Cys Ile Tyr Gly Ser His Thr Ala Gly
              95              100              105
CTC TCA GAG AGC AGT GAC CCC CTG GAG CTG GTG GTG ACA GGA GCC TAC      446
Leu Ser Glu Ser Ser Asp Pro Leu Glu Leu Val Val Thr Gly Ala Tyr
              110              115              120
AGC AAA CCC ACC CTC TCA GCT CTG CCC AGC CCT GTG GTG ACC TCA GGA      494
Ser Lys Pro Thr Leu Ser Ala Leu Pro Ser Pro Val Val Thr Ser Gly
              125              130              135
GGG AAT GTG ACC ATC CAG TGT GAC TCA CAG GTG GCA TTT GAT GGC TTC      542
Gly Asn Val Thr Ile Gln Cys Asp Ser Gln Val Ala Phe Asp Gly Phe
              140              145              150
ATT CTG TGT AAG GAA GGA GAA GAT GAA CAC CCA CAA TGC CTG AAC TCC      590
Ile Leu Cys Lys Glu Gly Glu Asp Glu His Pro Gln Cys Leu Asn Ser
              155              160              165              170
CAT TCC CAT GCC CGT GGG TCA TCC CGG GCC ATC TTC TCC GTG GGC CCC      638
```


His	Ser	His	Ala	Arg	Gly	Ser	Ser	Arg	Ala	Ile	Phe	Ser	Val	Gly	Pro	
				175					180					185		
GTG	AGC	CCA	AGT	CGC	AGG	TGG	TCG	TAC	AGG	TGC	TAT	GGT	TAT	GAC	TCG	686
Val	Ser	Pro	Ser	Arg	Arg	Trp	Ser	Tyr	Arg	Cys	Tyr	Gly	Tyr	Asp	Ser	
			190					195					200			
CGC	GCT	CCC	TAT	GTG	TGG	TCT	CTA	CCC	AGT	GAT	CTC	CTG	GGG	CTC	CTG	734
Arg	Ala	Pro	Tyr	Val	Trp	Ser	Leu	Pro	Ser	Asp	Leu	Leu	Gly	Leu	Leu	
		205					210					215				
GTC	CCA	GGT	GTT	TCT	AAG	AAG	CCA	TCA	CTC	TCA	GTG	CAG	CCG	GGT	CCT	782
Val	Pro	Gly	Val	Ser	Lys	Lys	Pro	Ser	Leu	Ser	Val	Gln	Pro	Gly	Pro	
	220					225					230					
GTC	GTG	GCC	CCT	GGG	GAG	AAG	CTG	ACC	TTC	CAG	TGT	GGC	TCT	GAT	GCC	830
Val	Val	Ala	Pro	Gly	Glu	Lys	Leu	Thr	Phe	Gln	Cys	Gly	Ser	Asp	Ala	
	235				240					245					250	
GGC	TAC	GAC	AGA	TTT	GTT	CTG	TAC	AAG	GAG	TGG	GGA	CGT	GAC	TTC	CTC	878
Gly	Tyr	Asp	Arg	Phe	Val	Leu	Tyr	Lys	Glu	Trp	Gly	Arg	Asp	Phe	Leu	
			255						260					265		
CAG	CGC	CCT	GGC	CGG	CAG	CCC	CAG	GCT	GGG	CTC	TCC	CAG	GCC	AAC	TTC	926
Gln	Arg	Pro	Gly	Arg	Gln	Pro	Gln	Ala	Gly	Leu	Ser	Gln	Ala	Asn	Phe	
			270					275					280			
ACC	CTG	GGC	CCT	GTG	AGC	CGC	TCC	TAC	GGG	GGC	CAG	TAC	ACA	TGC	TCC	974
Thr	Leu	Gly	Pro	Val	Ser	Arg	Ser	Tyr	Gly	Gly	Gln	Tyr	Thr	Cys	Ser	
		285					290					295				
GGT	GCA	TAC	AAC	CTC	TCC	TCC	GAG	TGG	TCG	GCC	CCC	AGC	GAC	CCC	CTG	1022
Gly	Ala	Tyr	Asn	Leu	Ser	Ser	Glu	Trp	Ser	Ala	Pro	Ser	Asp	Pro	Leu	
	300					305					310					
GAC	ATC	CTG	ATC	ACA	GGA	CAG	ATC	CGT	GCC	AGA	CCC	TTC	CTC	TCC	GTG	1070
Asp	Ile	Leu	Ile	Thr	Gly	Gln	Ile	Arg	Ala	Arg	Pro	Phe	Leu	Ser	Val	
	315				320				325						330	
CGG	CCG	GGC	CCC	ACA	GTG	GCC	TCA	GGA	GAG	AAC	GTG	ACC	CTG	CTG	TGT	1118
Arg	Pro	Gly	Pro	Thr	Val	Ala	Ser	Gly	Glu	Asn	Val	Thr	Leu	Leu	Cys	
				335					340					345		
CAG	TCA	CAG	GGA	GGG	ATG	CAC	ACT	TTC	CTT	TTG	ACC	AAG	GAG	GGG	GCA	1166
Gln	Ser	Gln	Gly	Gly	Met	His	Thr	Phe	Leu	Leu	Thr	Lys	Glu	Gly	Ala	
			350					355					360			
GCT	GAT	TCC	CCG	CTG	CGT	CTA	AAA	TCA	AAG	CGC	CAA	TCT	CAT	AAG	TAC	1214
Ala	Asp	Ser	Pro	Leu	Arg	Leu	Lys	Ser	Lys	Arg	Gln	Ser	His	Lys	Tyr	
		365					370					375				
CAG	GCT	GAA	TTC	CCC	ATG	AGT	CCT	GTG	ACC	TCG	GCC	CAC	GCG	GGG	ACC	1262
Gln	Ala	Glu	Phe	Pro	Met	Ser	Pro	Val	Thr	Ser	Ala	His	Ala	Gly	Thr	
	380						385				390					
TAC	AGG	TGC	TAC	GGC	TCA	CTC	AGC	TCC	AAC	CCC	TAC	CTG	CTG	ACT	CAC	1310
Tyr	Arg	Cys	Tyr	Gly	Ser	Leu	Ser	Ser	Asn	Pro	Tyr	Leu	Leu	Thr	His	
	395				400					405					410	

CCC AGT GAC CCC CTG GAG CTC GTG GTC TCA GGA GCA GCT GAG ACC CTC	1358
Pro Ser Asp Pro Leu Glu Leu Val Val Ser Gly Ala Ala Glu Thr Leu	
415 420 425	
AGC CCA CCA CAA AAC AAG TCC GAC TCC AAG GCT GGT GAG TGAGGAGATG	1407
Ser Pro Pro Gln Asn Lys Ser Asp Ser Lys Ala Gly Glu	
430 435	
CTTGCCGTGA TGACGCTGGG CACAGAGGGT CAGGTCCTGT CAAGAGGAGC TGGGTGTCCT	1467
GGGTGGACAT TTGAAGAATT ATATTCATTC CAACTTGAAG AATTATTCAA CACCTTTAAC	1527
AATGTATATG TGAAGTACTT TATTCTTTCA TATTTTAAAA ATAAAAGATA ATTATCCATG	1587
AAAAAAAAAA AAAAAAAAAA AAAGGGCGGC CGC	1620

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Thr	Pro	Ile	Leu	Thr	Val	Leu	Ile	Cys	Leu	Gly	Leu	Ser	Leu	Asp	1	5	10	15
Pro	Arg	Thr	His	Val	Gln	Ala	Gly	Pro	Leu	Pro	Lys	Pro	Thr	Leu	Trp	20	25	30	
Ala	Glu	Pro	Gly	Ser	Val	Ile	Thr	Gln	Gly	Ser	Pro	Val	Thr	Leu	Arg	35	40	45	
Cys	Gln	Gly	Ser	Leu	Glu	Thr	Gln	Glu	Tyr	His	Leu	Tyr	Arg	Glu	Lys	50	55	60	
Lys	Thr	Ala	Leu	Trp	Ile	Thr	Arg	Ile	Pro	Gln	Glu	Leu	Val	Lys	Lys	65	70	75	80
Gly	Gln	Phe	Pro	Ile	Leu	Ser	Ile	Thr	Trp	Glu	His	Ala	Gly	Arg	Tyr	85	90	95	
Cys	Cys	Ile	Tyr	Gly	Ser	His	Thr	Ala	Gly	Leu	Ser	Glu	Ser	Ser	Asp	100	105	110	
Pro	Leu	Glu	Leu	Val	Val	Thr	Gly	Ala	Tyr	Ser	Lys	Pro	Thr	Leu	Ser	115	120	125	
Ala	Leu	Pro	Ser	Pro	Val	Val	Thr	Ser	Gly	Gly	Asn	Val	Thr	Ile	Gln	130	135	140	
Cys	Asp	Ser	Gln	Val	Ala	Phe	Asp	Gly	Phe	Ile	Leu	Cys	Lys	Glu	Gly	145	150	155	160

Glu Asp Glu His Pro Gln Cys Leu Asn Ser His Ser His Ala Arg Gly
 165 170 175
 Ser Ser Arg Ala Ile Phe Ser Val Gly Pro Val Ser Pro Ser Arg Arg
 180 185 190
 Trp Ser Tyr Arg Cys Tyr Gly Tyr Asp Ser Arg Ala Pro Tyr Val Trp
 195 200 205
 Ser Leu Pro Ser Asp Leu Leu Gly Leu Leu Val Pro Gly Val Ser Lys
 210 215 220
 Lys Pro Ser Leu Ser Val Gln Pro Gly Pro Val Val Ala Pro Gly Glu
 225 230 235 240
 Lys Leu Thr Phe Gln Cys Gly Ser Asp Ala Gly Tyr Asp Arg Phe Val
 245 250 255
 Leu Tyr Lys Glu Trp Gly Arg Asp Phe Leu Gln Arg Pro Gly Arg Gln
 260 265 270
 Pro Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser
 275 280 285
 Arg Ser Tyr Gly Gly Gln Tyr Thr Cys Ser Gly Ala Tyr Asn Leu Ser
 290 295 300
 Ser Glu Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly
 305 310 315 320
 Gln Ile Arg Ala Arg Pro Phe Leu Ser Val Arg Pro Gly Pro Thr Val
 325 330 335
 Ala Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Gln Gly Gly Met
 340 345 350
 His Thr Phe Leu Leu Thr Lys Glu Gly Ala Ala Asp Ser Pro Leu Arg
 355 360 365
 Leu Lys Ser Lys Arg Gln Ser His Lys Tyr Gln Ala Glu Phe Pro Met
 370 375 380
 Ser Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser
 385 390 395 400
 Leu Ser Ser Asn Pro Tyr Leu Leu Thr His Pro Ser Asp Pro Leu Glu
 405 410 415
 Leu Val Val Ser Gly Ala Ala Glu Thr Leu Ser Pro Pro Gln Asn Lys
 420 425 430
 Ser Asp Ser Lys Ala Gly Glu
 435

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2197 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 191..1483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGACCCAC GCGTCCGGTC AACTTTTCTT CCCCTACTTC CCTGCATTTC TCCTCTGTGC	60
TCACTGCCAC ACGCAGCTCA ACCTGGACGG CACAGCCAGA TGCGAGATGC GTCTCTGCTG	120
ATCTGAGTCT GCCTGCAGCA TGGACCTGGG TCTTCCCTGA AGCATCTCCA GGGCTGGAGG	180
GACGACTGCC ATG CAC CGA GGG CTC ATC CAT CCG CAG AGC AGG GCA GTG	229
Met His Arg Gly Leu Ile His Pro Gln Ser Arg Ala Val	
1 5 10	
GGA GGA GAC GCC ATG ACC CCC ATC GTC ACA GTC CTG ATC TGT CTC GGG	277
Gly Gly Asp Ala Met Thr Pro Ile Val Thr Val Leu Ile Cys Leu Gly	
15 20 25	
CTG AGT CTG GGC CCC AGG ACC CAC GTG CAG ACA GGG ACC ATC CCC AAG	325
Leu Ser Leu Gly Pro Arg Thr His Val Gln Thr Gly Thr Ile Pro Lys	
30 35 40 45	
CCC ACC CTG TGG GCT GAG CCA GAC TCT GTG ATC ACC CAG GGG AGT CCC	373
Pro Thr Leu Trp Ala Glu Pro Asp Ser Val Ile Thr Gln Gly Ser Pro	
50 55 60	
GTC ACC CTC AGT TGT CAG GGG AGC CTT GAA GCC CAG GAG TAC CGT CTA	421
Val Thr Leu Ser Cys Gln Gly Ser Leu Glu Ala Gln Glu Tyr Arg Leu	
65 70 75	
TAT AGG GAG AAA AAA TCA GCA TCT TGG ATT ACA CGG ATA CGA CCA GAG	469
Tyr Arg Glu Lys Lys Ser Ala Ser Trp Ile Thr Arg Ile Arg Pro Glu	
80 85 90	
CTT GTG AAG AAC GGC CAG TTC CAC ATC CCA TCC ATC ACC TGG GAA CAC	517
Leu Val Lys Asn Gly Gln Phe His Ile Pro Ser Ile Thr Trp Glu His	
95 100 105	
ACA GGG CGA TAT GGC TGT CAG TAT TAC AGC CGC GCT CGG TGG TCT GAG	565
Thr Gly Arg Tyr Gly Cys Gln Tyr Tyr Ser Arg Ala Arg Trp Ser Glu	
110 115 120 125	
CTC AGT GAC CCC CTG GTG CTG GTG ATG ACA GGA GCC TAC CCA AAA CCC	613
Leu Ser Asp Pro Leu Val Leu Val Met Thr Gly Ala Tyr Pro Lys Pro	
130 135 140	
ACC CTC TCA GCC CAG CCC AGC CCT GTG GTG ACC TCA GGA GGA AGG GTG	661

Thr	Leu	Ser	Ala	Gln	Pro	Ser	Pro	Val	Val	Thr	Ser	Gly	Gly	Arg	Val	
			145					150					155			
ACC	CTC	CAG	TGT	GAG	TCA	CAG	GTG	GCA	TTT	GGC	GGC	TTC	ATT	CTG	TGT	709
Thr	Leu	Gln	Cys	Glu	Ser	Gln	Val	Ala	Phe	Gly	Gly	Phe	Ile	Leu	Cys	
		160					165					170				
AAG	GAA	GGA	GAA	GAT	GAA	CAC	CCA	CAA	TGC	CTG	AAC	TCC	CAG	CCC	CAT	757
Lys	Glu	Gly	Glu	Asp	Glu	His	Pro	Gln	Cys	Leu	Asn	Ser	Gln	Pro	His	
	175					180					185					
GCC	CGT	GGG	TCG	TCC	CGC	GCC	ATC	TTC	TCC	GTG	GGC	CCC	GTG	AGC	CCG	805
Ala	Arg	Gly	Ser	Ser	Arg	Ala	Ile	Phe	Ser	Val	Gly	Pro	Val	Ser	Pro	
190					195					200					205	
AAT	CGC	AGG	TGG	TCG	CAC	AGG	TGC	TAT	GGT	TAT	GAC	TTG	AAC	TCT	CCC	853
Asn	Arg	Arg	Trp	Ser	His	Arg	Cys	Tyr	Gly	Tyr	Asp	Leu	Asn	Ser	Pro	
			210					215						220		
TAT	GTG	TGG	TCT	TCA	CCC	AGT	GAT	CTC	CTG	GAG	CTC	CTG	GTC	CCA	GGT	901
Tyr	Val	Trp	Ser	Ser	Pro	Ser	Asp	Leu	Leu	Glu	Leu	Leu	Val	Pro	Gly	
			225					230					235			
GTT	TCT	AAG	AAG	CCA	TCA	CTC	TCA	GTG	CAG	CCG	GGT	CCT	GTC	GTG	GCC	949
Val	Ser	Lys	Lys	Pro	Ser	Leu	Ser	Val	Gln	Pro	Gly	Pro	Val	Val	Ala	
		240					245					250				
CCT	GGG	GAA	AGC	CTG	ACC	CTC	CAG	TGT	GTC	TCT	GAT	GTC	GGC	TAT	GAC	997
Pro	Gly	Glu	Ser	Leu	Thr	Leu	Gln	Cys	Val	Ser	Asp	Val	Gly	Tyr	Asp	
	255					260					265					
AGA	TTT	GTT	CTG	TAC	AAG	GAG	GGG	GAA	CGT	GAC	CTT	CGC	CAG	CTC	CCT	1045
Arg	Phe	Val	Leu	Tyr	Lys	Glu	Gly	Glu	Arg	Asp	Leu	Arg	Gln	Leu	Pro	
270					275					280					285	
GGC	CGG	CAG	CCC	CAG	GCT	GGG	CTC	TCC	CAG	GCC	AAC	TTC	ACC	CTG	GGC	1093
Gly	Arg	Gln	Pro	Gln	Ala	Gly	Leu	Ser	Gln	Ala	Asn	Phe	Thr	Leu	Gly	
				290					295					300		
CCT	GTG	AGC	CGC	TCC	TAC	GGG	GGC	CAG	TAC	AGA	TGC	TAC	GGT	GCA	TAC	1141
Pro	Val	Ser	Arg	Ser	Tyr	Gly	Gly	Gln	Tyr	Arg	Cys	Tyr	Gly	Ala	Tyr	
			305					310					315			
AAC	CTC	TCC	TCC	GAG	TGG	TCG	GCC	CCC	AGC	GAC	CCC	CTG	GAC	ATC	CTG	1189
Asn	Leu	Ser	Ser	Glu	Trp	Ser	Ala	Pro	Ser	Asp	Pro	Leu	Asp	Ile	Leu	
		320					325					330				
ATC	ACA	GGA	CAG	ATC	CAT	GGC	ACA	CCC	TTC	ATC	TCA	GTG	CAG	CCA	GGC	1237
Ile	Thr	Gly	Gln	Ile	His	Gly	Thr	Pro	Phe	Ile	Ser	Val	Gln	Pro	Gly	
	335					340					345					
CCC	ACA	GTG	GCC	TCA	GGA	GAG	AAC	GTG	ACC	CTG	CTG	TGT	CAG	TCA	TGG	1285
Pro	Thr	Val	Ala	Ser	Gly	Glu	Asn	Val	Thr	Leu	Leu	Cys	Gln	Ser	Trp	
350					355					360					365	
CGG	CAG	TTC	CAC	ACT	TTC	CTT	CTG	ACC	AAG	GCG	GGA	GCA	GCT	GAT	GCC	1333
Arg	Gln	Phe	His	Thr	Phe	Leu	Leu	Thr	Lys	Ala	Gly	Ala	Ala	Asp	Ala	
				370					375					380		

CCA CTC CGT CTA AGA TCA ATA CAC GAA TAT CCT AAG TAC CAG GCT GAA	1381
Pro Leu Arg Leu Arg Ser Ile His Glu Tyr Pro Lys Tyr Gln Ala Glu	
385 390 395	
TTC CCC ATG AGT CCT GTG ACC TCA GCC CAC GCG GGG ACC TAC AGG ACC	1429
Phe Pro Met Ser Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg Thr	
400 405 410	
CTC CAT GGG TTC CAG CCC CCC ACC CAC CGG TCC CAT CTC CAC ACC TGC	1477
Leu His Gly Phe Gln Pro Pro Thr His Arg Ser His Leu His Thr Cys	
415 420 425	
AGG CCC TGAGGACCAG CCCCTCACCC CCACTGGGTC GGATCCCCAA AGTGGTCTGG	1533
Arg Pro	
430	
GAAGGCACCT GGGGGTTGTG ATCGGCATCT TGGTGGCCGT CGTCCTACTG CTCCTCCTCC	1593
TCCTCCTCCT CTTCTCATC CTCCGACATC GACGTCAGGG CAAACACTGG ACATCGACCC	1653
AGAGAAAGGC TGATTTCCAA CATCCTGCAG GGGCTGTGGG GCCAGAGCCC ACAGACAGAG	1713
GCCTGCAGTG GAGGTCCAGC CCAGCTGCCG ACGCCCAGGA AGAAAACCTC TATGCTGCCG	1773
TGAAGGACAC ACAGCCTGAA GATGGGGTGG AGATGGACAC TCGGGCTGCT GCATCTGAAG	1833
CCCCCAGGA TGTGACCTAC GCCCAGCTGC ACAGCTTGAC CCTCAGACGG AAGGCAACTG	1893
AGCCTCCTCC ATCCCAGGAA AGGGAACCTC CAGCTGAGCC CAGCATTTAC GCCACCCTGG	1953
CCATCCACTA GCCCGGAGGG TACGCAGACT CCACACTCAG TAGAAGGAGA CTCAGGACTG	2013
CTGAAGGCAC GGGAGCTGCC CCCAGTGGAC ACCAATGAAC CCCAGTCAGC CTGGACCCCT	2073
AACAAAGACC ATGAGGAGAT GCTGGGAACT TTGGGACTCA CTTGATTCTG CAGTGGAAAT	2133
AACTAATATC CCTACATTTT TTAATTAAAG CAACAGACTT CTCAATAATC AATGAGTTAA	2193
CCGA	2197

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met His Arg Gly Leu Ile His Pro Gln Ser Arg Ala Val Gly Gly Asp
1 5 10 15
Ala Met Thr Pro Ile Val Thr Val Leu Ile Cys Leu Gly Leu Ser Leu
20 25 30

Gly Pro Arg Thr His Val Gln Thr Gly Thr Ile Pro Lys Pro Thr Leu
 35 40 45
 Trp Ala Glu Pro Asp Ser Val Ile Thr Gln Gly Ser Pro Val Thr Leu
 50 55 60
 Ser Cys Gln Gly Ser Leu Glu Ala Gln Glu Tyr Arg Leu Tyr Arg Glu
 65 70 75 80
 Lys Lys Ser Ala Ser Trp Ile Thr Arg Ile Arg Pro Glu Leu Val Lys
 85 90 95
 Asn Gly Gln Phe His Ile Pro Ser Ile Thr Trp Glu His Thr Gly Arg
 100 105 110
 Tyr Gly Cys Gln Tyr Tyr Ser Arg Ala Arg Trp Ser Glu Leu Ser Asp
 115 120 125
 Pro Leu Val Leu Val Met Thr Gly Ala Tyr Pro Lys Pro Thr Leu Ser
 130 135 140
 Ala Gln Pro Ser Pro Val Val Thr Ser Gly Gly Arg Val Thr Leu Gln
 145 150 155 160
 Cys Glu Ser Gln Val Ala Phe Gly Gly Phe Ile Leu Cys Lys Glu Gly
 165 170 175
 Glu Asp Glu His Pro Gln Cys Leu Asn Ser Gln Pro His Ala Arg Gly
 180 185 190
 Ser Ser Arg Ala Ile Phe Ser Val Gly Pro Val Ser Pro Asn Arg Arg
 195 200 205
 Trp Ser His Arg Cys Tyr Gly Tyr Asp Leu Asn Ser Pro Tyr Val Trp
 210 215 220
 Ser Ser Pro Ser Asp Leu Leu Glu Leu Leu Val Pro Gly Val Ser Lys
 225 230 235 240
 Lys Pro Ser Leu Ser Val Gln Pro Gly Pro Val Val Ala Pro Gly Glu
 245 250 255
 Ser Leu Thr Leu Gln Cys Val Ser Asp Val Gly Tyr Asp Arg Phe Val
 260 265 270
 Leu Tyr Lys Glu Gly Glu Arg Asp Leu Arg Gln Leu Pro Gly Arg Gln
 275 280 285
 Pro Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser
 290 295 300
 Arg Ser Tyr Gly Gly Gln Tyr Arg Cys Tyr Gly Ala Tyr Asn Leu Ser
 305 310 315 320
 Ser Glu Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly
 325 330 335

Gln Ile His Gly Thr Pro Phe Ile Ser Val Gln Pro Gly Pro Thr Val
 340 345 350
 Ala Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Trp Arg Gln Phe
 355 360 365
 His Thr Phe Leu Leu Thr Lys Ala Gly Ala Ala Asp Ala Pro Leu Arg
 370 375 380
 Leu Arg Ser Ile His Glu Tyr Pro Lys Tyr Gln Ala Glu Phe Pro Met
 385 390 395 400
 Ser Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg Thr Leu His Gly
 405 410 415
 Phe Gln Pro Pro Thr His Arg Ser His Leu His Thr Cys Arg Pro
 420 425 430

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 191..2035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTCGACCCAC GCGTCCGGTC AACTTTTCTT CCCCTACTTC CCTGCATTTT TCCTCTGTGC	60
TCACTGCCAC ACGCAGCTCA ACCTGGACGG CACAGCCAGA TGCGAGATGC GTCTCTGCTG	120
ATCTGAGTCT GCCTGCAGCA TGGACCTGGG TCTTCCCTGA AGCATCTCCA GGGCTGGAGG	180
GACGACTGCC ATG CAC CGA GGG CTC ATC CAT CCG CAG AGC AGG GCA GTG	229
Met His Arg Gly Leu Ile His Pro Gln Ser Arg Ala Val	
1 5 10	
GGA GGA GAC GCC ATG ACC CCC ATC GTC ACA GTC CTG ATC TGT CTC GGG	277
Gly Gly Asp Ala Met Thr Pro Ile Val Thr Val Leu Ile Cys Leu Gly	
15 20 25	
CTG AGT CTG GGC CCC AGG ACC CAC GTG CAG ACA GGG ACC ATC CCC AAG	325
Leu Ser Leu Gly Pro Arg Thr His Val Gln Thr Gly Thr Ile Pro Lys	
30 35 40 45	
CCC ACC CTG TGG GCT GAG CCA GAC TCT GTG ATC ACC CAG GGG AGT CCC	373
Pro Thr Leu Trp Ala Glu Pro Asp Ser Val Ile Thr Gln Gly Ser Pro	
50 55 60	

GTC ACC CTC AGT TGT CAG GGG AGC CTT GAA GCC CAG GAG TAC CGT CTA	421
Val Thr Leu Ser Cys Gln Gly Ser Leu Glu Ala Gln Glu Tyr Arg Leu	
65 70 75	
TAT AGG GAG AAA AAA TCA GCA TCT TGG ATT ACA CGG ATA CGA CCA GAG	469
Tyr Arg Glu Lys Lys Ser Ala Ser Trp Ile Thr Arg Ile Arg Pro Glu	
80 85 90	
CTT GTG AAG AAC GGC CAG TTC CAC ATC CCA TCC ATC ACC TGG GAA CAC	517
Leu Val Lys Asn Gly Gln Phe His Ile Pro Ser Ile Thr Trp Glu His	
95 100 105	
ACA GGG CGA TAT GGC TGT CAG TAT TAC AGC CGC GCT CGG TGG TCT GAG	565
Thr Gly Arg Tyr Gly Cys Gln Tyr Tyr Ser Arg Ala Arg Trp Ser Glu	
110 115 120 125	
CTC AGT GAC CCC CTG GTG CTG GTG ATG ACA GGA GCC TAC CCA AAA CCC	613
Leu Ser Asp Pro Leu Val Leu Val Met Thr Gly Ala Tyr Pro Lys Pro	
130 135 140	
ACC CTC TCA GCC CAG CCC AGC CCT GTG GTG ACC TCA GGA GGA AGG GTG	661
Thr Leu Ser Ala Gln Pro Ser Pro Val Val Thr Ser Gly Gly Arg Val	
145 150 155	
ACC CTC CAG TGT GAG TCA CAG GTG GCA TTT GGC GGC TTC ATT CTG TGT	709
Thr Leu Gln Cys Glu Ser Gln Val Ala Phe Gly Gly Phe Ile Leu Cys	
160 165 170	
AAG GAA GGA GAA GAT GAA CAC CCA CAA TGC CTG AAC TCC CAG CCC CAT	757
Lys Glu Gly Glu Asp Glu His Pro Gln Cys Leu Asn Ser Gln Pro His	
175 180 185	
GCC CGT GGG TCG TCC CGC GCC ATC TTC TCC GTG GGC CCC GTG AGC CCG	805
Ala Arg Gly Ser Ser Arg Ala Ile Phe Ser Val Gly Pro Val Ser Pro	
190 195 200 205	
AAT CGC AGG TGG TCG CAC AGG TGC TAT GGT TAT GAC TTG AAC TCT CCC	853
Asn Arg Arg Trp Ser His Arg Cys Tyr Gly Tyr Asp Leu Asn Ser Pro	
210 215 220	
TAT GTG TGG TCT TCA CCC AGT GAT CTC CTG GAG CTC CTG GTC CCA GGT	901
Tyr Val Trp Ser Ser Pro Ser Asp Leu Leu Glu Leu Leu Val Pro Gly	
225 230 235	
GTT TCT AAG AAG CCA TCA CTC TCA GTG CAG CCG GGT CCT GTC GTG GCC	949
Val Ser Lys Lys Pro Ser Leu Ser Val Gln Pro Gly Pro Val Val Ala	
240 245 250	
CCT GGG GAA AGC CTG ACC CTC CAG TGT GTC TCT GAT GTC GGC TAT GAC	997
Pro Gly Glu Ser Leu Thr Leu Gln Cys Val Ser Asp Val Gly Tyr Asp	
255 260 265	
AGA TTT GTT CTG TAC AAG GAG GGG GAA CGT GAC CTT CGC CAG CTC CCT	1045
Arg Phe Val Leu Tyr Lys Glu Gly Glu Arg Asp Leu Arg Gln Leu Pro	
270 275 280 285	
GGC CGG CAG CCC CAG GCT GGG CTC TCC CAG GCC AAC TTC ACC CTG GGC	1093
Gly Arg Gln Pro Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly	

[illegible]

GGG CCA GAG CCC ACA GAC AGA GGC CTG CAG TGG AGG TCC AGC CCA GCT	1813
Gly Pro Glu Pro Thr Asp Arg Gly Leu Gln Trp Arg Ser Ser Pro Ala	
530 535 540	
GCC GAC GCC CAG GAA GAA AAC CTC TAT GCT GCC GTG AAG GAC ACA CAG	1861
Ala Asp Ala Gln Glu Glu Asn Leu Tyr Ala Ala Val Lys Asp Thr Gln	
545 550 555	
CCT GAA GAT GGG GTG GAG ATG GAC ACT CGG GCT GCT GCA TCT GAA GCC	1909
Pro Glu Asp Gly Val Glu Met Asp Thr Arg Ala Ala Ala Ser Glu Ala	
560 565 570	
CCC CAG GAT GTG ACC TAC GCC CAG CTG CAC AGC TTG ACC CTC AGA CGG	1957
Pro Gln Asp Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg	
575 580 585	
AAG GCA ACT GAG CCT CCT CCA TCC CAG GAA AGG GAA CCT CCA GCT GAG	2005
Lys Ala Thr Glu Pro Pro Pro Ser Gln Glu Arg Glu Pro Pro Ala Glu	
590 595 600 605	
CCC AGC ATT TAC GCC ACC CTG GCC ATC CAC TAGCCCGGAG GGTACGCAGA	2055
Pro Ser Ile Tyr Ala Thr Leu Ala Ile His	
610 615	
CTCCACACTC AGTAGAAGGA GACTCAGGAC TGCTGAAGGC ACGGGAGCTG CCCCCAGTGG	2115
ACACCAATGA ACCCCAGTCA GCCTGGACCC CTAACAAAGA CCATGAGGAG ATGCTGGGAA	2175
CTTTGGGACT CACTTGATTC TGCAGTGGAA ATAACATAA TCCCTACATT TTTTAATTAA	2235
AGCAACAGAC TTCTCAATAA TCAATGAGTT AACCGA	2271

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met His Arg Gly Leu Ile His Pro Gln Ser Arg Ala Val Gly Gly Asp	
1 5 10 15	
Ala Met Thr Pro Ile Val Thr Val Leu Ile Cys Leu Gly Leu Ser Leu	
20 25 30	
Gly Pro Arg Thr His Val Gln Thr Gly Thr Ile Pro Lys Pro Thr Leu	
35 40 45	
Trp Ala Glu Pro Asp Ser Val Ile Thr Gln Gly Ser Pro Val Thr Leu	
50 55 60	
Ser Cys Gln Gly Ser Leu Glu Ala Gln Glu Tyr Arg Leu Tyr Arg Glu	
65 70 75 80	

Lys	Lys	Ser	Ala	Ser	Trp	Ile	Thr	Arg	Ile	Arg	Pro	Glu	Leu	Val	Lys
				85					90					95	
Asn	Gly	Gln	Phe	His	Ile	Pro	Ser	Ile	Thr	Trp	Glu	His	Thr	Gly	Arg
			100					105					110		
Tyr	Gly	Cys	Gln	Tyr	Tyr	Ser	Arg	Ala	Arg	Trp	Ser	Glu	Leu	Ser	Asp
		115					120					125			
Pro	Leu	Val	Leu	Val	Met	Thr	Gly	Ala	Tyr	Pro	Lys	Pro	Thr	Leu	Ser
	130					135					140				
Ala	Gln	Pro	Ser	Pro	Val	Val	Thr	Ser	Gly	Gly	Arg	Val	Thr	Leu	Gln
145					150					155					160
Cys	Glu	Ser	Gln	Val	Ala	Phe	Gly	Gly	Phe	Ile	Leu	Cys	Lys	Glu	Gly
				165					170					175	
Glu	Asp	Glu	His	Pro	Gln	Cys	Leu	Asn	Ser	Gln	Pro	His	Ala	Arg	Gly
			180					185					190		
Ser	Ser	Arg	Ala	Ile	Phe	Ser	Val	Gly	Pro	Val	Ser	Pro	Asn	Arg	Arg
		195					200					205			
Trp	Ser	His	Arg	Cys	Tyr	Gly	Tyr	Asp	Leu	Asn	Ser	Pro	Tyr	Val	Trp
	210					215					220				
Ser	Ser	Pro	Ser	Asp	Leu	Leu	Glu	Leu	Leu	Val	Pro	Gly	Val	Ser	Lys
225					230					235					240
Lys	Pro	Ser	Leu	Ser	Val	Gln	Pro	Gly	Pro	Val	Val	Ala	Pro	Gly	Glu
				245					250					255	
Ser	Leu	Thr	Leu	Gln	Cys	Val	Ser	Asp	Val	Gly	Tyr	Asp	Arg	Phe	Val
			260					265					270		
Leu	Tyr	Lys	Glu	Gly	Glu	Arg	Asp	Leu	Arg	Gln	Leu	Pro	Gly	Arg	Gln
	275						280					285			
Pro	Gln	Ala	Gly	Leu	Ser	Gln	Ala	Asn	Phe	Thr	Leu	Gly	Pro	Val	Ser
	290					295						300			
Arg	Ser	Tyr	Gly	Gly	Gln	Tyr	Arg	Cys	Tyr	Gly	Ala	Tyr	Asn	Leu	Ser
305					310					315					320
Ser	Glu	Trp	Ser	Ala	Pro	Ser	Asp	Pro	Leu	Asp	Ile	Leu	Ile	Thr	Gly
				325					330					335	
Gln	Ile	His	Gly	Thr	Pro	Phe	Ile	Ser	Val	Gln	Pro	Gly	Pro	Thr	Val
			340					345					350		
Ala	Ser	Gly	Glu	Asn	Val	Thr	Leu	Leu	Cys	Gln	Ser	Trp	Arg	Gln	Phe
		355					360					365			
His	Thr	Phe	Leu	Leu	Thr	Lys	Ala	Gly	Ala	Ala	Asp	Ala	Pro	Leu	Arg
	370					375					380				

Leu Arg Ser Ile His Glu Tyr Pro Lys Tyr Gln Ala Glu Phe Pro Met
 385 390 395 400
 Ser Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser
 405 410 415
 Leu Asn Ser Asp Pro Tyr Leu Leu Ser His Pro Ser Glu Pro Leu Glu
 420 425 430
 Leu Val Val Ser Gly Pro Ser Met Gly Ser Ser Pro Pro Pro Thr Gly
 435 440 445
 Pro Ile Ser Thr Pro Ala Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr
 450 455 460
 Gly Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val Val Ile
 465 470 475 480
 Gly Ile Leu Val Ala Val Val Leu Leu Leu Leu Leu Leu Leu Leu
 485 490 495
 Phe Leu Ile Leu Arg His Arg Arg Gln Gly Lys His Trp Thr Ser Thr
 500 505 510
 Gln Arg Lys Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly Pro Glu
 515 520 525
 Pro Thr Asp Arg Gly Leu Gln Trp Arg Ser Ser Pro Ala Ala Asp Ala
 530 535 540
 Gln Glu Glu Asn Leu Tyr Ala Ala Val Lys Asp Thr Gln Pro Glu Asp
 545 550 555 560
 Gly Val Glu Met Asp Thr Arg Ala Ala Ala Ser Glu Ala Pro Gln Asp
 565 570 575
 Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg Lys Ala Thr
 580 585 590
 Glu Pro Pro Pro Ser Gln Glu Arg Glu Pro Pro Ala Glu Pro Ser Ile
 595 600 605
 Tyr Ala Thr Leu Ala Ile His
 610 615

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 180..2024

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AAAGAAGTCA ACTTTTCTTC CCCTACTTCC CTGCATTTCT CCTCTGTGCT CACTGCCACA	60
CGCAGCTCAA CCTGGACGGC ACAGCCAGAT GCGAGATGCG TCTCTGCTGA TCTGAGTCTG	120
CCTGCAGCAT GGACCTGGGT CTTCCCTGAA GCATCTCCAG GGCTGGAGGG ACGACTGCC	179
ATG CAC CGA GGG CTC ATC CAT CCG CAG AGC AGG GCA GTG GGA GGA GAC	227
Met His Arg Gly Leu Ile His Pro Gln Ser Arg Ala Val Gly Gly Asp	
1 5 10 15	
GCC ATG ACC CCC ATC GTC ACA GTC CTG ATC TGT CTC GGG CTG AGT CTG	275
Ala Met Thr Pro Ile Val Thr Val Leu Ile Cys Leu Gly Leu Ser Leu	
20 25 30	
GGC CCC AGG ACC CAC GTG CAG ACA GGG ACC ATC CCC AAG CCC ACC CTG	323
Gly Pro Arg Thr His Val Gln Thr Gly Thr Ile Pro Lys Pro Thr Leu	
35 40 45	
TGG GCT GAG CCA GAC TCT GTG ATC ACC CAG GGG AGT CCC GTC ACC CTC	371
Trp Ala Glu Pro Asp Ser Val Ile Thr Gln Gly Ser Pro Val Thr Leu	
50 55 60	
AGT TGT CAG GGG AGC CTT GAA GCC CAG GAG TAC CGT CTA TAT AGG GAG	419
Ser Cys Gln Gly Ser Leu Glu Ala Gln Glu Tyr Arg Leu Tyr Arg Glu	
65 70 75 80	
AAA AAA TCA GCA TCT TGG ATT ACA CGG ATA CGA CCA GAG CTT GTG AAG	467
Lys Lys Ser Ala Ser Trp Ile Thr Arg Ile Arg Pro Glu Leu Val Lys	
85 90 95	
AAC GGC CAG TTC CAC ATC CCA TCC ATC ACC TGG GAA CAC ACA GGG CGA	515
Asn Gly Gln Phe His Ile Pro Ser Ile Thr Trp Glu His Thr Gly Arg	
100 105 110	
TAT GGC TGT CAG TAT TAC AGC CGC GCT CGG TGG TCT GAG CTC AGT GAC	563
Tyr Gly Cys Gln Tyr Tyr Ser Arg Ala Arg Trp Ser Glu Leu Ser Asp	
115 120 125	
CCC CTG GTG CTG GTG ATG ACA GGA GCC TAC CCA AAA CCC ACC CTC TCA	611
Pro Leu Val Leu Val Met Thr Gly Ala Tyr Pro Lys Pro Thr Leu Ser	
130 135 140	
GCC CAG CCC AGC CCT GTG GTG ACC TCA GGA GGA AGG GTG ACC CTC CAG	659
Ala Gln Pro Ser Pro Val Val Thr Ser Gly Gly Arg Val Thr Leu Gln	
145 150 155 160	
TGT GAG TCA CAG GTG GCA TTT GGC GGC TTC ATT CTG TGT AAG GAA GGA	707
Cys Glu Ser Gln Val Ala Phe Gly Gly Phe Ile Leu Cys Lys Glu Gly	
165 170 175	
GAA GAT GAA CAC CCA CAA TGC CTG AAC TCC CAG CCC CAT GCC CGT GGG	755
Glu Asp Glu His Pro Gln Cys Leu Asn Ser Gln Pro His Ala Arg Gly	
180 185 190	

TCG	TCC	CGC	GCC	ATC	TTC	TCC	GTG	GGC	CCC	GTG	AGC	CCG	AAT	CGC	AGG	803
Ser	Ser	Arg	Ala	Ile	Phe	Ser	Val	Gly	Pro	Val	Ser	Pro	Asn	Arg	Arg	
		195					200					205				
TGG	TCG	CAC	AGG	TGC	TAT	GGT	TAT	GAC	TTG	AAC	TCT	CCC	TAT	GTG	TGG	851
Trp	Ser	His	Arg	Cys	Tyr	Gly	Tyr	Asp	Leu	Asn	Ser	Pro	Tyr	Val	Trp	
	210					215					220					
TCT	TCA	CCC	AGT	GAT	CTC	CTG	GAG	CTC	CTG	GTC	CCA	GGT	GTT	TCT	AAG	899
Ser	Ser	Pro	Ser	Asp	Leu	Leu	Glu	Leu	Leu	Val	Pro	Gly	Val	Ser	Lys	
225					230					235					240	
AAG	CCA	TCA	CTC	TCA	GTG	CAG	CCG	GGT	CCT	GTC	GTG	GCC	CCT	GGG	GAA	947
Lys	Pro	Ser	Leu	Ser	Val	Gln	Pro	Gly	Pro	Val	Val	Ala	Pro	Gly	Glu	
			245					250						255		
AGC	CTG	ACC	CTC	CAG	TGT	GTC	TCT	GAT	GTC	GGC	TAT	GAC	AGA	TTT	GTT	995
Ser	Leu	Thr	Leu	Gln	Cys	Val	Ser	Asp	Val	Gly	Tyr	Asp	Arg	Phe	Val	
			260					265					270			
CTG	TAC	AAG	GAG	GGG	GAA	CGT	GAC	CTT	CGC	CAG	CTC	CCT	GGC	CGG	CAG	1043
Leu	Tyr	Lys	Glu	Gly	Glu	Arg	Asp	Leu	Arg	Gln	Leu	Pro	Gly	Arg	Gln	
	275						280					285				
CCC	CAG	GCT	GGG	CTC	TCC	CAG	GCC	AAC	TTC	ACC	CTG	GGC	CCT	GTG	AGC	1091
Pro	Gln	Ala	Gly	Leu	Ser	Gln	Ala	Asn	Phe	Thr	Leu	Gly	Pro	Val	Ser	
	290					295					300					
CGC	TCC	TAC	GGG	GGC	CAG	TAC	AGA	TGC	TAC	GGT	GCA	TAC	AAC	CTC	TCC	1139
Arg	Ser	Tyr	Gly	Gly	Gln	Tyr	Arg	Cys	Tyr	Gly	Ala	Tyr	Asn	Leu	Ser	
305					310					315					320	
TCC	GAG	TGG	TCG	GCC	CCC	AGC	GAC	CCC	CTG	GAC	ATC	CTG	ATC	ACA	GGA	1187
Ser	Glu	Trp	Ser	Ala	Pro	Ser	Asp	Pro	Leu	Asp	Ile	Leu	Ile	Thr	Gly	
			325					330						335		
CAG	ATC	CAT	GGC	ACA	CCC	TTC	ATC	TCA	GTG	CAG	CCA	GGC	CCC	ACA	GTG	1235
Gln	Ile	His	Gly	Thr	Pro	Phe	Ile	Ser	Val	Gln	Pro	Gly	Pro	Thr	Val	
			340				345					350				
GCC	TCA	GGA	GAG	AAC	GTG	ACC	CTG	CTG	TGT	CAG	TCA	TGG	CGG	CAG	TTC	1283
Ala	Ser	Gly	Glu	Asn	Val	Thr	Leu	Leu	Cys	Gln	Ser	Trp	Arg	Gln	Phe	
		355					360					365				
CAC	ACT	TTC	CTT	CTG	ACC	AAG	GCG	GGA	GCA	GCT	GAT	GCC	CCA	CTC	CGT	1331
His	Thr	Phe	Leu	Leu	Thr	Lys	Ala	Gly	Ala	Ala	Asp	Ala	Pro	Leu	Arg	
	370					375					380					
CTA	AGA	TCA	ATA	CAC	GAA	TAT	CCT	AAG	TAC	CAG	GCT	GAA	TTC	CCC	ATG	1379
Leu	Arg	Ser	Ile	His	Glu	Tyr	Pro	Lys	Tyr	Gln	Ala	Glu	Phe	Pro	Met	
385					390					395					400	
AGT	CCC	GTG	ACC	TCA	GCC	CAC	GCG	GGG	ACC	TAC	AGG	TGC	TAC	GGC	TCA	1427
Ser	Pro	Val	Thr	Ser	Ala	His	Ala	Gly	Thr	Tyr	Arg	Cys	Tyr	Gly	Ser	
			405					410						415		
CTC	AAC	TCC	GAC	CCC	TAC	CTG	CTG	TCT	CAC	CCC	AGT	GAG	CCC	CTG	GAG	1475

Leu Asn Ser Asp Pro Tyr Leu Leu Ser His Pro Ser Glu Pro Leu Glu	
420 425 430	
CTC GTG GTC TCA GGA CCC TCC ATG GGT TCC AGC CCC CCA CCC ACC GGT	1523
Leu Val Val Ser Gly Pro Ser Met Gly Ser Ser Pro Pro Thr Gly	
435 440 445	
CCC ATC TCC ACA CCT GCA GGC CCT GAG GAC CAG CCC CTC ACC CCC ACT	1571
Pro Ile Ser Thr Pro Ala Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr	
450 455 460	
GGG TCG GAT CCC CAA AGT GGT CTG GGA AGG CAC CTG GGG GTT GTG ATC	1619
Gly Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val Val Ile	
465 470 475 480	
GGC ATC TTG GTG GCC GTC GTC CTA CTG CTC CTC CTC CTC CTC CTC CTC	1667
Gly Ile Leu Val Ala Val Val Leu Leu Leu Leu Leu Leu Leu Leu Leu	
485 490 495	
TTC CTC ATC CTC CGA CAT CGA CGT CAG GGC AAA CAC TGG ACA TCG ACC	1715
Phe Leu Ile Leu Arg His Arg Arg Gln Gly Lys His Trp Thr Ser Thr	
500 505 510	
CAG AGA AAG GCT GAT TTC CAA CAT CCT GCA GGG GCT GTG GGG CCA GAG	1763
Gln Arg Lys Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly Pro Glu	
515 520 525	
CCC ACA GAC AGA GGC CTG CAG TGG AGG TCC AGC CCA GCT GCC GAC GCC	1811
Pro Thr Asp Arg Gly Leu Gln Trp Arg Ser Ser Pro Ala Ala Asp Ala	
530 535 540	
CAG GAA GAA AAC CTC TAT GCT GCC GTG AAG GAC ACA CAG CCT GAA GAT	1859
Gln Glu Glu Asn Leu Tyr Ala Ala Val Lys Asp Thr Gln Pro Glu Asp	
545 550 555 560	
GGG GTG GAG ATG GAC ACT CGG GCT GCT GCA TCT GAA GCC CCC CAG GAT	1907
Gly Val Glu Met Asp Thr Arg Ala Ala Ala Ser Glu Ala Pro Gln Asp	
565 570 575	
GTG ACC TAC GCC CAG CTG CAC AGC TTG ACC CTC AGA CGG AAG GCA ACT	1955
Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg Lys Ala Thr	
580 585 590	
GAG CCT CCT CCA TCC CAG GAA AGG GAA CCT CCA GCT GAG CCC AGC ATC	2003
Glu Pro Pro Pro Ser Gln Glu Glu Glu Pro Pro Ala Glu Pro Ser Ile	
595 600 605	
TAC GCC ACC CTG GCC ATC CAC TAGCCCGGAG GGTACGCAGA CTCCACACTC	2054
Tyr Ala Thr Leu Ala Ile His	
610 615	
AGTAGAAGGA GACTCAGGAC TGCTGAAGGC ACGGGAGCTG CCCCCAGTGG ACACCAATGA	2114
ACCCCAGTCA GCCTGGACCC CTAACAAAGA CCATGAGGAG ATGCTGGGAA CTTTGGGACT	2174
CACTTGATTG TGCAGTCGAA ATAACATAATA TCCCTACATT TTTTAATTAA AGCAACAGAC	2234
TTCTCAATAA TCAATGAGTT AACCGAGAAA ACTAAAATCA GAAGTAAGAA TGTGCTTTAA	2294

ACTGAATCAC AATATAAATA TTACACATCA CACAATGAAA TTGAAAAAGT ACAAACCACA 2354
AATGAAAAAA GTAGAAACGA AAAAAAAAAA AAAA 2388

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	His	Arg	Gly	Leu	Ile	His	Pro	Gln	Ser	Arg	Ala	Val	Gly	Gly	Asp	1	5	10	15
Ala	Met	Thr	Pro	Ile	Val	Thr	Val	Leu	Ile	Cys	Leu	Gly	Leu	Ser	Leu	20	25	30	
Gly	Pro	Arg	Thr	His	Val	Gln	Thr	Gly	Thr	Ile	Pro	Lys	Pro	Thr	Leu	35	40	45	
Trp	Ala	Glu	Pro	Asp	Ser	Val	Ile	Thr	Gln	Gly	Ser	Pro	Val	Thr	Leu	50	55	60	
Ser	Cys	Gln	Gly	Ser	Leu	Glu	Ala	Gln	Glu	Tyr	Arg	Leu	Tyr	Arg	Glu	65	70	75	80
Lys	Lys	Ser	Ala	Ser	Trp	Ile	Thr	Arg	Ile	Arg	Pro	Glu	Leu	Val	Lys	85	90	95	
Asn	Gly	Gln	Phe	His	Ile	Pro	Ser	Ile	Thr	Trp	Glu	His	Thr	Gly	Arg	100	105	110	
Tyr	Gly	Cys	Gln	Tyr	Tyr	Ser	Arg	Ala	Arg	Trp	Ser	Glu	Leu	Ser	Asp	115	120	125	
Pro	Leu	Val	Leu	Val	Met	Thr	Gly	Ala	Tyr	Pro	Lys	Pro	Thr	Leu	Ser	130	135	140	
Ala	Gln	Pro	Ser	Pro	Val	Val	Thr	Ser	Gly	Gly	Arg	Val	Thr	Leu	Gln	145	150	155	160
Cys	Glu	Ser	Gln	Val	Ala	Phe	Gly	Gly	Phe	Ile	Leu	Cys	Lys	Glu	Gly	165	170	175	
Glu	Asp	Glu	His	Pro	Gln	Cys	Leu	Asn	Ser	Gln	Pro	His	Ala	Arg	Gly	180	185	190	
Ser	Ser	Arg	Ala	Ile	Phe	Ser	Val	Gly	Pro	Val	Ser	Pro	Asn	Arg	Arg	195	200	205	
Trp	Ser	His	Arg	Cys	Tyr	Gly	Tyr	Asp	Leu	Asn	Ser	Pro	Tyr	Val	Trp	210	215	220	

Ser Ser Pro Ser Asp Leu Leu Glu Leu Leu Val Pro Gly Val Ser Lys
 225 230 235 240
 Lys Pro Ser Leu Ser Val Gln Pro Gly Pro Val Val Ala Pro Gly Glu
 245 250 255
 Ser Leu Thr Leu Gln Cys Val Ser Asp Val Gly Tyr Asp Arg Phe Val
 260 265 270
 Leu Tyr Lys Glu Gly Glu Arg Asp Leu Arg Gln Leu Pro Gly Arg Gln
 275 280 285
 Pro Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser
 290 295 300
 Arg Ser Tyr Gly Gly Gln Tyr Arg Cys Tyr Gly Ala Tyr Asn Leu Ser
 305 310 315 320
 Ser Glu Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly
 325 330 335
 Gln Ile His Gly Thr Pro Phe Ile Ser Val Gln Pro Gly Pro Thr Val
 340 345 350
 Ala Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Trp Arg Gln Phe
 355 360 365
 His Thr Phe Leu Leu Thr Lys Ala Gly Ala Ala Asp Ala Pro Leu Arg
 370 375 380
 Leu Arg Ser Ile His Glu Tyr Pro Lys Tyr Gln Ala Glu Phe Pro Met
 385 390 395 400
 Ser Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser
 405 410 415
 Leu Asn Ser Asp Pro Tyr Leu Leu Ser His Pro Ser Glu Pro Leu Glu
 420 425 430
 Leu Val Val Ser Gly Pro Ser Met Gly Ser Ser Pro Pro Pro Thr Gly
 435 440 445
 Pro Ile Ser Thr Pro Ala Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr
 450 455 460
 Gly Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val Val Ile
 465 470 475 480
 Gly Ile Leu Val Ala Val Val Leu Leu Leu Leu Leu Leu Leu Leu Leu
 485 490 495
 Phe Leu Ile Leu Arg His Arg Arg Gln Gly Lys His Trp Thr Ser Thr
 500 505 510
 Gln Arg Lys Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly Pro Glu
 515 520 525

Pro Thr Asp Arg Gly Leu Gln Trp Arg Ser Ser Pro Ala Ala Asp Ala
530 535 540

Gln Glu Glu Asn Leu Tyr Ala Ala Val Lys Asp Thr Gln Pro Glu Asp
545 550 555 560

Gly Val Glu Met Asp Thr Arg Ala Ala Ala Ser Glu Ala Pro Gln Asp
565 570 575

Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg Lys Ala Thr
580 585 590

Glu Pro Pro Pro Ser Gln Glu Arg Glu Pro Pro Ala Glu Pro Ser Ile
595 600 605

Tyr Ala Thr Leu Ala Ile His
610 615

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 174..1466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTCAACTTTT CTTCCCCTAC TTCCCTGCAT TTCTCCTCTG TGCTCACTGC CACACGCAGC 60

TCAACCTGGA CGGCACAGCC AGATGCGAGA TCGTCTCTG CTGATCTGAG TCTGCCTGCA 120

GCATGGACCT GGGTCTTCCC TGAAGCATCT CCAGGGCTGG AGGGACGACT GCC ATG 176
Met
1

CAC CGA GGG CTC ATC CAT CCG CAG AGC AGG GCA GTG GGA GGA GAC GCC 224
His Arg Gly Leu Ile His Pro Gln Ser Arg Ala Val Gly Gly Asp Ala
5 10 15

ATG ACC CCC ATC GTC ACA GTC CTG ATC TGT CTC GGG CTG AGT CTG GGC 272
Met Thr Pro Ile Val Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Gly
20 25 30

CCC AGG ACC CAC GTG CAG ACA GGG ACC ATC CCC AAG CCC ACC CTG TGG 320
Pro Arg Thr His Val Gln Thr Gly Thr Ile Pro Lys Pro Thr Leu Trp
35 40 45

GCT GAG CCA GAC TCT GTG ATC ACC CAG GGG AGT CCC GTC ACC CTC AGT 368
Ala Glu Pro Asp Ser Val Ile Thr Gln Gly Ser Pro Val Thr Leu Ser

50	55	60	65	
TGT CAG GGG AGC CTT GAA GCC CAG GAG TAC CGT CTA TAT AGG GAG AAA Cys Gln Gly Ser Leu Glu Ala Gln Glu Tyr Arg Leu Tyr Arg Glu Lys	70	75	80	416
AAA TCA GCA TCT TGG ATT ACA CGG ATA CGA CCA GAG CTT GTG AAG AAC Lys Ser Ala Ser Trp Ile Thr Arg Ile Arg Pro Glu Leu Val Lys Asn	85	90	95	464
GGC CAG TTC CAC ATC CCA TCC ATC ACC TGG GAA CAC ACA GGG CGA TAT Gly Gln Phe His Ile Pro Ser Ile Thr Trp Glu His Thr Gly Arg Tyr	100	105	110	512
GGC TGT CAG TAT TAC AGC CGC GCT CGG TGG TCT GAG CTC AGT GAC CCC Gly Cys Gln Tyr Tyr Ser Arg Ala Arg Trp Ser Glu Leu Ser Asp Pro	115	120	125	560
CTG GTG CTG GTG ATG ACA GGA GCC TAC CCA AAA CCC ACC CTC TCA GCC Leu Val Leu Val Met Thr Gly Ala Tyr Pro Lys Pro Thr Leu Ser Ala	130	135	140	608
CAG CCC AGC CCT GTG GTG ACC TCA GGA GGA AGG GTG ACC CTC CAG TGT Gln Pro Ser Pro Val Val Thr Ser Gly Gly Arg Val Thr Leu Gln Cys	150	155	160	656
GAG TCA CAG GTG GCA TTT GGC GGC TTC ATT CTG TGT AAG GAA GGA GAA Glu Ser Gln Val Ala Phe Gly Gly Phe Ile Leu Cys Lys Glu Gly Glu	165	170	175	704
GAT GAA CAC CCA CAA TGC CTG AAC TCC CAG CCC CAT GCC CGT GGG TCG Asp Glu His Pro Gln Cys Leu Asn Ser Gln Pro His Ala Arg Gly Ser	180	185	190	752
TCC CGC GCC ATC TTC TCC GTG GGC CCC GTG AGC CCG AAT CGC AGG TGG Ser Arg Ala Ile Phe Ser Val Gly Pro Val Ser Pro Asn Arg Arg Trp	195	200	205	800
TCG CAC AGG TGC TAT GGT TAT GAC TTG AAC TCT CCC TAT GTG TGG TCT Ser His Arg Cys Tyr Gly Tyr Asp Leu Asn Ser Pro Tyr Val Trp Ser	210	215	220	848
TCA CCC AGT GAT CTC CTG GAG CTC CTG GTC CCA GGT GTT TCT AAG AAG Ser Pro Ser Asp Leu Leu Glu Leu Leu Val Pro Gly Val Ser Lys Lys	230	235	240	896
CCA TCA CTC TCA GTG CAG CCG GGT CCT GTC GTG GCC CCT GGG GAA AGC Pro Ser Leu Ser Val Gln Pro Gly Pro Val Val Ala Pro Gly Glu Ser	245	250	255	944
CTG ACC CTC CAG TGT GTC TCT GAT GTC GGC TAT GAC AGA TTT GTT CTG Leu Thr Leu Gln Cys Val Ser Asp Val Gly Tyr Asp Arg Phe Val Leu	260	265	270	992
TAC AAG GAG GGG GAA CGT GAC CTT CGC CAG CTC CCT GGC CGG CAG CCC Tyr Lys Glu Gly Glu Arg Asp Leu Arg Gln Leu Pro Gly Arg Gln Pro	275	280	285	1040

CAG GCT GGG CTC TCC CAG GCC AAC TTC ACC CTG GGC CCT GTG AGC CGC Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser Arg 290 295 300 305	1088
TCC TAC GGG GGC CAG TAC AGA TGC TAC GGT GCA TAC AAC CTC TCC TCC Ser Tyr Gly Gly Gln Tyr Arg Cys Tyr Gly Ala Tyr Asn Leu Ser Ser 310 315 320	1136
GAG TGG TCG GCC CCC AGC GAC CCC CTG GAC ATC CTG ATC ACA GGA CAG Glu Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Thr Gly Gln 325 330 335	1184
ATC CAT GGC ACA CCC TTC ATC TCA GTG CAG CCA GGC CCC ACA GTG GCC Ile His Gly Thr Pro Phe Ile Ser Val Gln Pro Gly Pro Thr Val Ala 340 345 350	1232
TCA GGA GAG AAC GTG ACC CTG CTG TGT CAG TCA TGG CGG CAG TTC CAC Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Trp Arg Gln Phe His 355 360 365	1280
ACT TTC CTT CTG ACC AAG GCG GGA GCA GCT GAT GCC CCA CTC CGT CTA Thr Phe Leu Leu Thr Lys Ala Gly Ala Ala Asp Ala Pro Leu Arg Leu 370 375 380 385	1328
AGA TCA ATA CAC GAA TAT CCT AAG TAC CAG GCT GAA TTC CCC ATG AGT Arg Ser Ile His Glu Tyr Pro Lys Tyr Gln Ala Glu Phe Pro Met Ser 390 395 400	1376
CCT GTG ACC TCA GCC CAC GCG GGG ACC TAC AGG ACC CTC CAT GGG TTC Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg Thr Leu His Gly Phe 405 410 415	1424
CAG CCC CCC ACC CAC CGG TCC CAT CTC CAC ACC TGC AGG CCC Gln Pro Pro Thr His Arg Ser His Leu His Thr Cys Arg Pro 420 425 430	1466
TGAGGACCAG CCCCTCACCC CCACTGGGTC GGATCCCCAA AGTGGTCTGG GAAGGCACCT	1526
GGGGGTGTG ATCGGCATCT TGGTGGCCGT CGTCCTACTG CTCCTCCTCC TCCTCCTCCT	1586
CTTCCTCATC CTCCGACATC GACGTCAGGG CAAACACTGG ACATCGACCC AGAGAAAGGC	1646
TGATTTCCAA CATCCTGCAG GGGCTGTGGG GCCAGAGCCC ACAGACAGAG GCCTGCAGTG	1706
GAGGTCCAGC CCAGCTGCCG ACGCCCAGGA AGAAAACCTC TATGCTGCCG TGAAGGACAC	1766
ACAGCCTGAA GATGGGGTGG AGATGGACAC TCGGGCTGCT GCATCTGAAG CCCCCAGGA	1826
TGTGACCTAC GCCCAGCTGC ACAGCTTGAC CCTCAGACGG AAGGCAACTG AGCCTCCTCC	1886
ATCCCAGGAA AGGGAACCTC CAGCTGAGCC CAGCATCTAC GCCACCCTGG CCATCCACTA	1946
GCCCGGAGGG TACGCAGACT CCACACTCAG TAGAAGGAGA CTCAGGACTG CTGAAGGCAC	2006
GGGAGCTGCC CCCAGTGGAC ACCAATGAAC CCCAGTCAGC CTGGACCCCT AACAAAGACC	2066
ATGAGGAGAT GCTGGGAAC TTGGGACTCA CTTGATTCTG CAGTCGAAAT AACTAATATC	2126

CCTACATTTT TTAATTAAAG CAACAGACTT CTCAATAATC AATGAGTTAA CCGAGAAAAC 2186
TAAAAAAAAA AAAA 2200

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	His	Arg	Gly	Leu	Ile	His	Pro	Gln	Ser	Arg	Ala	Val	Gly	Gly	Asp	1	5	10	15
Ala	Met	Thr	Pro	Ile	Val	Thr	Val	Leu	Ile	Cys	Leu	Gly	Leu	Ser	Leu	20	25	30	
Gly	Pro	Arg	Thr	His	Val	Gln	Thr	Gly	Thr	Ile	Pro	Lys	Pro	Thr	Leu	35	40	45	
Trp	Ala	Glu	Pro	Asp	Ser	Val	Ile	Thr	Gln	Gly	Ser	Pro	Val	Thr	Leu	50	55	60	
Ser	Cys	Gln	Gly	Ser	Leu	Glu	Ala	Gln	Glu	Tyr	Arg	Leu	Tyr	Arg	Glu	65	70	75	80
Lys	Lys	Ser	Ala	Ser	Trp	Ile	Thr	Arg	Ile	Arg	Pro	Glu	Leu	Val	Lys	85	90	95	
Asn	Gly	Gln	Phe	His	Ile	Pro	Ser	Ile	Thr	Trp	Glu	His	Thr	Gly	Arg	100	105	110	
Tyr	Gly	Cys	Gln	Tyr	Tyr	Ser	Arg	Ala	Arg	Trp	Ser	Glu	Leu	Ser	Asp	115	120	125	
Pro	Leu	Val	Leu	Val	Met	Thr	Gly	Ala	Tyr	Pro	Lys	Pro	Thr	Leu	Ser	130	135	140	
Ala	Gln	Pro	Ser	Pro	Val	Val	Thr	Ser	Gly	Gly	Arg	Val	Thr	Leu	Gln	145	150	155	160
Cys	Glu	Ser	Gln	Val	Ala	Phe	Gly	Gly	Phe	Ile	Leu	Cys	Lys	Glu	Gly	165	170	175	
Glu	Asp	Glu	His	Pro	Gln	Cys	Leu	Asn	Ser	Gln	Pro	His	Ala	Arg	Gly	180	185	190	
Ser	Ser	Arg	Ala	Ile	Phe	Ser	Val	Gly	Pro	Val	Ser	Pro	Asn	Arg	Arg	195	200	205	
Trp	Ser	His	Arg	Cys	Tyr	Gly	Tyr	Asp	Leu	Asn	Ser	Pro	Tyr	Val	Trp	210	215	220	

Ser	Ser	Pro	Ser	Asp	Leu	Leu	Glu	Leu	Leu	Val	Pro	Gly	Val	Ser	Lys
225					230					235					240
Lys	Pro	Ser	Leu	Ser	Val	Gln	Pro	Gly	Pro	Val	Val	Ala	Pro	Gly	Glu
				245					250					255	
Ser	Leu	Thr	Leu	Gln	Cys	Val	Ser	Asp	Val	Gly	Tyr	Asp	Arg	Phe	Val
			260					265					270		
Leu	Tyr	Lys	Glu	Gly	Glu	Arg	Asp	Leu	Arg	Gln	Leu	Pro	Gly	Arg	Gln
		275					280					285			
Pro	Gln	Ala	Gly	Leu	Ser	Gln	Ala	Asn	Phe	Thr	Leu	Gly	Pro	Val	Ser
	290						295				300				
Arg	Ser	Tyr	Gly	Gly	Gln	Tyr	Arg	Cys	Tyr	Gly	Ala	Tyr	Asn	Leu	Ser
305					310					315				320	
Ser	Glu	Trp	Ser	Ala	Pro	Ser	Asp	Pro	Leu	Asp	Ile	Leu	Ile	Thr	Gly
				325					330					335	
Gln	Ile	His	Gly	Thr	Pro	Phe	Ile	Ser	Val	Gln	Pro	Gly	Pro	Thr	Val
			340					345					350		
Ala	Ser	Gly	Glu	Asn	Val	Thr	Leu	Leu	Cys	Gln	Ser	Trp	Arg	Gln	Phe
		355					360					365			
His	Thr	Phe	Leu	Leu	Thr	Lys	Ala	Gly	Ala	Ala	Asp	Ala	Pro	Leu	Arg
	370					375					380				
Leu	Arg	Ser	Ile	His	Glu	Tyr	Pro	Lys	Tyr	Gln	Ala	Glu	Phe	Pro	Met
385					390					395					400
Ser	Pro	Val	Thr	Ser	Ala	His	Ala	Gly	Thr	Tyr	Arg	Thr	Leu	His	Gly
				405					410					415	
Phe	Gln	Pro	Pro	Thr	His	Arg	Ser	His	Leu	His	Thr	Cys	Arg	Pro	
			420					425					430		

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 177..2132

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1722
- (D) OTHER INFORMATION: /note= "nucleotide 1722 designated

C, may be A, C, G, or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCCACACGCA GCTCAGCCTG GCGGCACAG CCAGATGCGA GATGCGTCTC TGCTGATCTG	60
AGTCTGCCTG CAGCATGGAC CTGGGTCTTC CCTGAAGCAT CTCCAGGGCT GGAGGGACGA	120
CTGCCATGCA CCGAGGGCTC ATCCATCCAC AGAGCAGGGC AGTGGGAGGA GACGCC	176
ATG ACC CCC ATC CTC ACG GTC CTG ATC TGT CTC GGG CTG AGT CTG GGC	224
Met Thr Pro Ile Leu Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Gly	
1 5 10 15	
CCC CGG ACC CAC GTG CAG GCA GGG CAC CTC CCC AAG CCC ACC CTC TGG	272
Pro Arg Thr His Val Gln Ala Gly His Leu Pro Lys Pro Thr Leu Trp	
20 25 30	
GCT GAA CCA GGC TCT GTG ATC ACC CAG GGG AGT CCT GTG ACC CTC AGG	320
Ala Glu Pro Gly Ser Val Ile Thr Gln Gly Ser Pro Val Thr Leu Arg	
35 40 45	
TGT CAG GGG GGC CAG GAG ACC CAG GAG TAC CGT CTA TAT AGA GAA AAG	368
Cys Gln Gly Gly Gln Glu Thr Gln Glu Tyr Arg Leu Tyr Arg Glu Lys	
50 55 60	
AAA ACA GCA CCC TGG ATT ACA CGG ATC CCA CAG GAG CTT GTG AAG AAG	416
Lys Thr Ala Pro Trp Ile Thr Arg Ile Pro Gln Glu Leu Val Lys Lys	
65 70 75 80	
GGC CAG TTC CCC ATC CCA TCC ATC ACC TGG GAA CAT GCA GGG CGG TAT	464
Gly Gln Phe Pro Ile Pro Ser Ile Thr Trp Glu His Ala Gly Arg Tyr	
85 90 95	
CGC TGT TAC TAT GGT AGC GAC ACT GCA GGC CGC TCA GAG AGC AGT GAC	512
Arg Cys Tyr Tyr Gly Ser Asp Thr Ala Gly Arg Ser Glu Ser Ser Asp	
100 105 110	
CCC CTG GAG CTG GTG GTG ACA GGA GCC TAC ATC AAA CCC ACC CTC TCA	560
Pro Leu Glu Leu Val Val Thr Gly Ala Tyr Ile Lys Pro Thr Leu Ser	
115 120 125	
GCC CAG CCC AGC CCC GTG GTG AAC TCA GGA GGG AAT GTA ACC CTC CAG	608
Ala Gln Pro Ser Pro Val Val Asn Ser Gly Gly Asn Val Thr Leu Gln	
130 135 140	
TGT GAC TCA CAG GTG GCA TTT GAT GGC TTC ATT CTG TGT AAG GAA GGA	656
Cys Asp Ser Gln Val Ala Phe Asp Gly Phe Ile Leu Cys Lys Glu Gly	
145 150 155 160	
GAA GAT GAA CAC CCA CAA TGC CTG AAC TCC CAG CCC CAT GCC CGT GGG	704
Glu Asp Glu His Pro Gln Cys Leu Asn Ser Gln Pro His Ala Arg Gly	
165 170 175	
TCG TCC CGC GCC ATC TTC TCC GTG GGC CCC GTG AGC CCG AGT CGC AGG	752
Ser Ser Arg Ala Ile Phe Ser Val Gly Pro Val Ser Pro Ser Arg Arg	
180 185 190	

TGG	TGG	TAC	AGG	TGC	TAT	GCT	TAT	GAC	TCG	AAC	TCT	CCC	TAT	GAG	TGG	800
Trp	Trp	Tyr	Arg	Cys	Tyr	Ala	Tyr	Asp	Ser	Asn	Ser	Pro	Tyr	Glu	Trp	
		195					200					205				
TCT	CTA	CCC	AGT	GAT	CTC	CTG	GAG	CTC	CTG	GTC	CTA	GGT	GTT	TCT	AAG	848
Ser	Leu	Pro	Ser	Asp	Leu	Leu	Glu	Leu	Leu	Val	Leu	Gly	Val	Ser	Lys	
	210					215					220					
AAG	CCA	TCA	CTC	TCA	GTG	CAG	CCA	GGT	CCT	ATC	GTG	GCC	CCT	GAG	GAG	896
Lys	Pro	Ser	Leu	Ser	Val	Gln	Pro	Gly	Pro	Ile	Val	Ala	Pro	Glu	Glu	
225					230					235					240	
ACC	CTG	ACT	CTG	CAG	TGT	GGC	TCT	GAT	GCT	GGC	TAC	AAC	AGA	TTT	GTT	944
Thr	Leu	Thr	Leu	Gln	Cys	Gly	Ser	Asp	Ala	Gly	Tyr	Asn	Arg	Phe	Val	
				245					250					255		
CTG	TAT	AAG	GAC	GGG	GAA	CGT	GAC	TTC	CTT	CAG	CTC	GCT	GGC	GCA	CAG	992
Leu	Tyr	Lys	Asp	Gly	Glu	Arg	Asp	Phe	Leu	Gln	Leu	Ala	Gly	Ala	Gln	
			260					265					270			
CCC	CAG	GCT	GGG	CTC	TCC	CAG	GCC	AAC	TTC	ACC	CTG	GGC	CCT	GTG	AGC	1040
Pro	Gln	Ala	Gly	Leu	Ser	Gln	Ala	Asn	Phe	Thr	Leu	Gly	Pro	Val	Ser	
		275					280					285				
CGC	TCC	TAC	GGG	GGC	CAG	TAC	AGA	TGC	TAC	GGT	GCA	CAC	AAC	CTC	TCC	1088
Arg	Ser	Tyr	Gly	Gly	Gln	Tyr	Arg	Cys	Tyr	Gly	Ala	His	Asn	Leu	Ser	
		290				295					300					
TCC	GAG	TGG	TCG	GCC	CCC	AGC	GAC	CCC	CTG	GAC	ATC	CTG	ATC	GCA	GGA	1136
Ser	Glu	Trp	Ser	Ala	Pro	Ser	Asp	Pro	Leu	Asp	Ile	Leu	Ile	Ala	Gly	
305					310					315					320	
CAG	TTC	TAT	GAC	AGA	GTC	TCC	CTC	TCG	GTG	CAG	CCG	GGC	CCC	ACG	GTG	1184
Gln	Phe	Tyr	Asp	Arg	Val	Ser	Leu	Ser	Val	Gln	Pro	Gly	Pro	Thr	Val	
				325					330					335		
GCC	TCA	GGA	GAG	AAC	GTG	ACC	CTG	CTG	TGT	CAG	TCA	CAG	GGA	TGG	ATG	1232
Ala	Ser	Gly	Glu	Asn	Val	Thr	Leu	Leu	Cys	Gln	Ser	Gln	Gly	Trp	Met	
			340					345					350			
CAA	ACT	TTC	CTT	CTG	ACC	AAG	GAG	GGG	GCA	GCT	GAT	GAC	CCA	TGG	CGT	1280
Gln	Thr	Phe	Leu	Leu	Thr	Lys	Glu	Gly	Ala	Ala	Asp	Asp	Pro	Trp	Arg	
		355					360					365				
CTA	AGA	TCA	ACG	TAC	CAA	TCT	CAA	AAA	TAC	CAG	GCT	GAA	TTC	CCC	ATG	1328
Leu	Arg	Ser	Thr	Tyr	Gln	Ser	Gln	Lys	Tyr	Gln	Ala	Glu	Phe	Pro	Met	
	370					375					380					
GGT	CCT	GTG	ACC	TCA	GCC	CAT	GCG	GGG	ACC	TAC	AGG	TGC	TAC	GGC	TCA	1376
Gly	Pro	Val	Thr	Ser	Ala	His	Ala	Gly	Thr	Tyr	Arg	Cys	Tyr	Gly	Ser	
385					390					395					400	
CAG	AGC	TCC	AAA	CCC	TAC	CTG	CTG	ACT	CAC	CCC	AGT	GAC	CCC	CTG	GAG	1424
Gln	Ser	Ser	Lys	Pro	Tyr	Leu	Leu	Thr	His	Pro	Ser	Asp	Pro	Leu	Glu	
				405					410					415		
CTC	GTG	GTC	TCA	GGA	CCG	TCT	GGG	GGC	CCC	AGC	TCC	CCG	ACA	ACA	GGC	1472

GACGCAGACC CCACACTCCA TGGAGTCTGG AATGCATGGG AGCTGCCCCC CCAGTGGACA	2202
CCATTGGACC CCACCCAGCC TGGATCTACC CCAGGAGACT CTGGGAACTT TTAGGGGTCA	2262
CTCAATTCTG CAGTATAAAT AACTAATGTC TCTACAATTT TGAAATAAAG CAACAGACTT	2322
CTCAATAATC AATGAAGTAG CTGAGAAAAC TAAGTCAGAA AGTGCATTAA ACTGAATCAC	2382
AATGTAAATA TTACACATCA AGCGATGAAA CTGGAAAACCT ACAAGCCACG AATGAATGAA	2442
TTAGGAAAGA AAAAAAGTAG GAAATGAATG ATCTTGGCTT TCCTATAAGA AATTTAGGGC	2502
AGGGCACGGT GGCTCACGCC TGTAATTCCA GCACTTTGGG AGGCCGAGGC GGGCAGATCA	2562
CGAGTTCAGG AGATCGAGAC CATCTTGGCC AACATGGTGA AACCCTGTCT CTCCTAAAAA	2622
TACAAAAATT AGCTGGATGT GGTGGCAGTG CCTGTAATCC CAGCTATTTG GGAGGCTGAG	2682
GCAGGAGAAT CGCTTGAACC AGGGAGTCAG AGGTTTCAGT GAGCCAAGAT CGCACCAC TG	2742
CTCTCCAGCC TGGCGACAGA GGGAGACTCC ATCTCAAATT AAAAAAAAAA	2790

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Thr Pro Ile Leu Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Gly	
1 5 10 15	
Pro Arg Thr His Val Gln Ala Gly His Leu Pro Lys Pro Thr Leu Trp	
20 25 30	
Ala Glu Pro Gly Ser Val Ile Thr Gln Gly Ser Pro Val Thr Leu Arg	
35 40 45	
Cys Gln Gly Gly Gln Glu Thr Gln Glu Tyr Arg Leu Tyr Arg Glu Lys	
50 55 60	
Lys Thr Ala Pro Trp Ile Thr Arg Ile Pro Gln Glu Leu Val Lys Lys	
65 70 75 80	
Gly Gln Phe Pro Ile Pro Ser Ile Thr Trp Glu His Ala Gly Arg Tyr	
85 90 95	
Arg Cys Tyr Tyr Gly Ser Asp Thr Ala Gly Arg Ser Glu Ser Ser Asp	
100 105 110	
Pro Leu Glu Leu Val Val Thr Gly Ala Tyr Ile Lys Pro Thr Leu Ser	
115 120 125	

Ala	Gln	Pro	Ser	Pro	Val	Val	Asn	Ser	Gly	Gly	Asn	Val	Thr	Leu	Gln	130	135	140
Cys	Asp	Ser	Gln	Val	Ala	Phe	Asp	Gly	Phe	Ile	Leu	Cys	Lys	Glu	Gly	145	150	155
Glu	Asp	Glu	His	Pro	Gln	Cys	Leu	Asn	Ser	Gln	Pro	His	Ala	Arg	Gly	165	170	175
Ser	Ser	Arg	Ala	Ile	Phe	Ser	Val	Gly	Pro	Val	Ser	Pro	Ser	Arg	Arg	180	185	190
Trp	Trp	Tyr	Arg	Cys	Tyr	Ala	Tyr	Asp	Ser	Asn	Ser	Pro	Tyr	Glu	Trp	195	200	205
Ser	Leu	Pro	Ser	Asp	Leu	Leu	Glu	Leu	Leu	Val	Leu	Gly	Val	Ser	Lys	210	215	220
Lys	Pro	Ser	Leu	Ser	Val	Gln	Pro	Gly	Pro	Ile	Val	Ala	Pro	Glu	Glu	225	230	235
Thr	Leu	Thr	Leu	Gln	Cys	Gly	Ser	Asp	Ala	Gly	Tyr	Asn	Arg	Phe	Val	245	250	255
Leu	Tyr	Lys	Asp	Gly	Glu	Arg	Asp	Phe	Leu	Gln	Leu	Ala	Gly	Ala	Gln	260	265	270
Pro	Gln	Ala	Gly	Leu	Ser	Gln	Ala	Asn	Phe	Thr	Leu	Gly	Pro	Val	Ser	275	280	285
Arg	Ser	Tyr	Gly	Gly	Gln	Tyr	Arg	Cys	Tyr	Gly	Ala	His	Asn	Leu	Ser	290	295	300
Ser	Glu	Trp	Ser	Ala	Pro	Ser	Asp	Pro	Leu	Asp	Ile	Leu	Ile	Ala	Gly	305	310	315
Gln	Phe	Tyr	Asp	Arg	Val	Ser	Leu	Ser	Val	Gln	Pro	Gly	Pro	Thr	Val	325	330	335
Ala	Ser	Gly	Glu	Asn	Val	Thr	Leu	Leu	Cys	Gln	Ser	Gln	Gly	Trp	Met	340	345	350
Gln	Thr	Phe	Leu	Leu	Thr	Lys	Glu	Gly	Ala	Ala	Asp	Asp	Pro	Trp	Arg	355	360	365
Leu	Arg	Ser	Thr	Tyr	Gln	Ser	Gln	Lys	Tyr	Gln	Ala	Glu	Phe	Pro	Met	370	375	380
Gly	Pro	Val	Thr	Ser	Ala	His	Ala	Gly	Thr	Tyr	Arg	Cys	Tyr	Gly	Ser	385	390	395
Gln	Ser	Ser	Lys	Pro	Tyr	Leu	Leu	Thr	His	Pro	Ser	Asp	Pro	Leu	Glu	405	410	415
Leu	Val	Val	Ser	Gly	Pro	Ser	Gly	Gly	Pro	Ser	Ser	Pro	Thr	Thr	Gly	420	425	430

Pro Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly
435 440 445

S r Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val Val Ile Gly
450 455 460

Ile Leu Val Ala Val Ile Leu Leu Leu Leu Leu Leu Leu Leu Phe
465 470 475 480

Leu Ile Leu Arg His Arg Arg Gln Gly Lys His Trp Thr Ser Thr Gln
485 490 495

Arg Lys Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly Pro Glu Pro
500 505 510

Thr Asp Arg Arg Leu Gln Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln
515 520 525

Glu Glu Asn Leu Tyr Ala Ala Val Lys His Thr Gln Pro Glu Asp Gly
530 535 540

Val Glu Met Asp Thr Arg Gln Ser Pro His Asp Glu Asp Pro Gln Ala
545 550 555 560

Val Thr Tyr Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu Met Ala
565 570 575

Ser Pro Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg
580 585 590

Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu
595 600 605

Ala Pro Gln Asp Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg
610 615 620

Arg Lys Ala Thr Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser Pro Ala
625 630 635 640

Val Pro Ser Ile Tyr Ala Thr Leu Ala Ile His *
645 650